



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160341

TO: Minh-Tam Davis
Location: REM-3A24&3C18
Art Unit: 1642
Thursday, July 28, 2005
Case Serial Number: 09/967305

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

RUSH

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 10:42:00 ; Search time 841 Seconds
(without alignments)
8811.362 Million cell updates/sec

Title: US-09-967-305-3

Perfect score: 1146

Sequence: 1 atggcactgcaggcatctc.....ataagtaaaagctagtctc 1146

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 7277826 seqs, 3233139505 residues

Word size: 0

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1146	100.0	1146	9	US-09-967-305-3
2	1146	100.0	2005	9	US-09-967-305-1
3	1146	100.0	2005	9	US-09-967-305-10
4	1146	100.0	2005	16	US-10-210-120-104
5	1146	100.0	2005	22	US-10-909-035-104
6	1146	100.0	2069	9	US-09-967-305-4
7	1146	100.0	2069	15	US-10-205-823-17

need print out

8	1132	98.8	3654	9	US-09-967-305-6	Sequence 6, Appli
9	1132	98.8	3654	15	US-10-205-823-19	Sequence 19, Appli
10	1095	95.5	2069	15	US-10-205-823-25	Sequence 25, Appli
11	1081	94.3	2626	15	US-10-205-823-27	Sequence 27, Appli
12	1070	93.4	1621	9	US-09-759-143-107	Sequence 107, App
13	1070	93.4	1621	9	US-09-780-669-107	Sequence 107, App
14	1070	93.4	1621	9	US-09-030-606-107	Sequence 107, App
15	1070	93.4	1621	9	US-09-822-827-107	Sequence 107, App
16	1070	93.4	1621	9	US-09-115-453-107	Sequence 107, App
17	1070	93.4	1621	9	US-09-232-880-107	Sequence 107, App
18	1070	93.4	1621	9	US-09-895-793-107	Sequence 107, App
19	1070	93.4	1621	9	US-09-895-814-107	Sequence 107, App
20	1070	93.4	1621	13	US-10-012-896-107	Sequence 107, App
21	1070	93.4	1621	14	US-10-010-940-107	Sequence 107, App
22	1070	93.4	1621	16	US-10-144-678A-107	Sequence 107, App
23	1070	93.4	1621	16	US-10-294-025-107	Sequence 107, App
24	1070	93.4	1621	19	US-10-688-838-107	Sequence 107, App
25	1070	93.4	2376	20	US-10-357-930-21284	Sequence 21284, A
26	1070	93.4	2376	20	US-10-357-930-21872	Sequence 21872, A
27	1070	93.4	2376	20	US-10-357-930-25228	Sequence 25228, A
28	1070	93.4	2376	20	US-10-357-930-27126	Sequence 27126, A
29	797	69.5	1294	20	US-10-357-930-22613	Sequence 22613, A
30	797	69.5	1294	20	US-10-357-930-22726	Sequence 22726, A
31	797	69.5	1294	20	US-10-357-930-27725	Sequence 27725, A
32	797	69.5	1294	20	US-10-357-930-28455	Sequence 28455, A
33	797	69.5	1294	20	US-10-357-930-28557	Sequence 28557, A
34	756	66.0	1039	17	US-10-378-029-3	Sequence 3, Appli
35	740	64.6	1316	15	US-10-205-823-23	Sequence 23, Appli
36	595	51.9	2946	15	US-10-205-823-29	Sequence 29, Appli
37	595	51.9	2946	19	US-10-316-540-13	Sequence 13, Appli
38	595	51.9	3023	9	US-09-967-305-8	Sequence 8, Appli
39	595	51.9	3023	15	US-10-205-823-21	Sequence 21, Appli
40	498	43.5	729	19	US-10-316-540-12	Sequence 12, Appli
41	493	43.0	865	20	US-10-357-930-20524	Sequence 20524, A
42	493	43.0	865	20	US-10-357-930-26361	Sequence 26361, A
43	493	43.0	865	20	US-10-357-930-28573	Sequence 28573, A
44	493	43.0	865	20	US-10-357-930-28729	Sequence 28729, A
45	493	43.0	1805	10	US-09-814-353-21605	Sequence 21605, A

ALIGNMENTS

US-09-967-305-3
; Sequence 3, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1146)
US-09-967-305-3

Query Match 100.0%; Score 1146; DB 9; Length 1146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGGCAGTGCAGGAGCATCTGCTGTGAGCTGTCTCCGGCCTGGCCCGGCGTCTGT 60

Db 1 ATGGCACTGCAGGGCATCTCGGTCGTGAGCTGTCCGGCTCGGCCCGGGCCGTTCTGT 60
QY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAACCGGCCGCTCCGC 120
Db 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAACCGGCCGCTCCGC 120
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
QY 181 CGGGGAGCCCGCGTGTGCTGCGCGCTGTGTGCAAGCGGTGGAATGTGCTGTGAGCCCTTC 240
Db 181 CGGGGAGCCCGCGTGTGCTGCGCGCTGTGTGCAAGCGGTGGAATGTGCTGTGAGCCCTTC 240
QY 241 CGCCGCGGTGCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
Db 241 CGCCGCGGTGCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
QY 301 AGGCTATTATGACCAGGCTGAGATTGGCCAGTCAAGAACTTCTGCGGTTAGCT 360
Db 301 AGGCTATTATGACCAGGCTGAGATTGGCCAGTCAAGAACTTCTGCGGTTAGCT 360
QY 361 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTGGCAGAGTGT 420
Db 361 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTGGCAGAGTGT 420
QY 421 GAGAAATCCGTATGCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTGCTGTATGT 480
Db 421 GAGAAATCCGTATGCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTGCTGTATGT 480
QY 481 GCACTGGGCATTATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
Db 481 GCACTGGGCATTATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
QY 541 GATGCAAAATATGTGGAAGAACACATATTTAAGTCTTTCTGTGAAAACCTCAGAAA 600
Db 541 GATGCAAAATATGTGGAAGAACACATATTTAAGTCTTTCTGTGAAAACCTCAGAAA 600
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGTGAGACACCTTTCTAT 660
Db 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGTGAGACACCTTTCTAT 660
QY 661 ACCGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCAATT 720
Db 661 ACCGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCAATT 720
QY 721 TACGAGCTGCTGATCAAAAGACTTGAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 721 TACGAGCTGCTGATCAAAAGACTTGAAGTCTGATGAATCTCCCAATCAGATGAGC 780
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGAGATGTATTGCAAGAAGACGAG 840
Db 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGAGATGTATTGCAAGAAGACGAG 840
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGAACCTCCGTTCTGACTTTT 900
Db 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGAACCTCCGTTCTGACTTTT 900
QY 901 GAGGAGGTGTTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAAGTAGAG 960
Db 901 GAGGAGGTGTTTCATCATGATCAACAAGGAACGGGGCTGTTTATCACCAAGTAGAG 960
QY 961 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 961 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
QY 1021 AAAAGGATCCTTTATAGAGAACACACTGAGAGATATTGAAGATTGGATTGAGC 1080
Db 1021 AAAAGGATCCTTTATAGAGAACACACTGAGAGATATTGAAGATTGGATTGAGC 1080
QY 1081 CGCGAAGAGATTATCAGCTTAAGTAAATCATTTGAAGTAATAGTTAAAGCT 1140
Db 1081 CGCGAAGAGATTATCAGCTTAAGTAAATCATTTGAAGTAATAGTTAAAGCT 1140

Db 1081 CGCGAAGAGATTATCAGCTTAAGTAAATCATTTGAAGTAATAGTTAAAGCT 1140
QY 1141 AGTCTC 1146
Db 1141 AGTCTC 1146

RESULT 2
US-09-967-305-1
; Sequence 1, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-305-1

Query Match 100.0%; Score 1146; DB 9; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCGTGAGCTGTCCGGCTCGGCCCGGGCCGTTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTCGTGAGCTGTCCGGCTCGGCCCGGGCCGTTCTGT 125
QY 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAACCGGCCGCTCCGC 120
Db 126 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAACCGGCCGCTCCGC 185
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db 186 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 245
QY 181 CGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240
Db 246 CGGGGAGCCCGCTGCTGCGCGCTGTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 305
QY 241 CGCCGCGGTGCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
Db 306 CGCCGCGGTGCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 365
QY 301 AGGCTATTATGACCAGGCTGAGTTGGCCAGTCAAGAACTTCTGCGGTTAGCT 360
Db 366 AGGCTATTATGACCAGGCTGAGTTGGCCAGTCAAGAACTTCTGCGGTTAGCT 425
QY 361 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTGGCAGAGTGT 420
Db 426 GGGCAGCATATCACTATTGGCTTGTCTCAGGTGTCTCTCAAAAATTGGCAGAGTGT 485
QY 421 GAGAAATCCGTATGCCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCTTATGTGT 480
Db 486 GAGAAATCCGTATGCCCCGCTGAATCTCTGCTGACTTTGCTGTGTGGCTTATGTGT 545
QY 481 GCACTGGGCATTATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAGTCAAT 540
Db 546 GCACTGGGCATTATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAGTCAAT 605
QY 541 GATGCAAAATATGTGGAAGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAAA 600
Db 606 GATGCAAAATATGTGGAAGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAAA 665

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGTTGAGCACCCTTTCTAT 660
|||
Db 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGTTGAGCACCCTTTCTAT 725
QY 661 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTTC 720
|||
Db 726 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTTC 785
QY 721 TACGAGCTGTGATCAAAAGACTTGAAGTCTGATGAAGTCTCCCAATCAGATGAGC 780
|||
Db 786 TACGAGCTGTGATCAAAAGACTTGAAGTCTGATGAAGTCTCCCAATCAGATGAGC 845
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATGTAATTTGCAAGAAGACGAAG 840
|||
Db 846 ATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATGTAATTTGCAAGAAGACGAAG 905
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTAATCCGGTTCTGACTTTT 900
|||
Db 906 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTAATCCGGTTCTGACTTTT 965
QY 901 GAGAGGTGTTCATCATGATCAACAAGAACGGGCTCGTTTATCACAGTAGAGAG 960
|||
Db 966 GAGAGGTGTTCATCATGATCAACAAGAACGGGCTCGTTTATCACAGTAGAGAG 1025
QY 961 CAGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
|||
Db 1026 CAGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTTGAAGAATTTGGATTACG 1080
|||
Db 1086 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTTGAAGAATTTGGATTACG 1145
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1140
|||
Db 1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1205
QY 1141 AGTCTC 1146
|||
Db 1206 AGTCTC 1211

RESULT 3
US-09-967-305-10
; Sequence 10, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(1211)
US-09-967-305-10

Query Match 100.0%; Score 1146; DB 9; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCACTGCAAGGCATCTCGTCTGTGAGCTGTCCGGCCTGGCCCGGGCCGTTCTGT 60
|||
Db 66 ATGCACTGCAAGGCATCTCGTCTGTGAGCTGTCCGGCCTGGCCCGGGCCGTTCTGT 125

QY 61 GCTATGTCCTGCTGACTTCGGGGCGCGTGTGTAAGCTGGACCGGCCGCTCCCGC 120
|||
Db 126 GCTATGTCCTGCTGACTTCGGGGCGCGTGTGTAAGCTGGACCGGCCGCTCCCGC 185
QY 121 TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGACCGG 180
|||
Db 186 TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGACCGG 245
QY 181 CGGGAGCCCGCGTCTGCGGCGTCTGTGCAAGCGGTCGGAATGTGCTGTGAGCCCTTC 240
|||
Db 246 CGGGAGCCCGCGTCTGCGGCGTCTGTGCAAGCGGTCGGAATGTGCTGTGAGCCCTTC 305
QY 241 CGCCCGGTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCTGACGGGAAATCCA 300
|||
Db 306 CGCCCGGTGTCAATGAGAACTCCAGCTGGGCCAGAGATTCTGACGGGAAATCCA 365
QY 301 AGGCTATTATGCAAGCTGAGTGAATTTGGCCAGTCAAGAACTTCTGCGGTTAGCT 360
|||
Db 366 AGGCTATTATGCAAGCTGAGTGAATTTGGCCAGTCAAGAACTTCTGCGGTTAGCT 425
QY 361 GGGCAGATATCAACTATTGGCTTGTGAGTGTCTCAAAATGSCAGAGTGT 420
|||
Db 426 GGGCAGATATCAACTATTGGCTTGTGAGTGTCTCAAAATGSCAGAGTGT 485
QY 421 GAGAAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTATGT 480
|||
Db 486 GAGAAATCCGTATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTATGT 545
QY 481 GCACTGGGCAATTATATGCTCTTTTGAACCGCACACGACTGGCAAGGTCAGTCAAT 540
|||
Db 546 GCACTGGGCAATTATATGCTCTTTTGAACCGCACACGACTGGCAAGGTCAGTCAAT 605
QY 541 GATGCAAAATATGTTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAA 600
|||
Db 606 GATGCAAAATATGTTGAAGGAACAGCATATTTAAGTCTTTCTGTGAAAACCTCAGAA 665
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTTGAGCACCCTTTCTAT 660
|||
Db 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGATGTTGAGCACCCTTTCTAT 725
QY 661 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTTC 720
|||
Db 726 ACGACTTACAGACAGACAGATGGGAATTGCTGTTGGACCAATAGAACCCAGTTTC 785
QY 721 TACGAGCTGTGATCAAAAGACTTGAAGTCTGATGAAGTCTCCCAATCAGATGAGC 780
|||
Db 786 TACGAGCTGTGATCAAAAGACTTGAAGTCTGATGAAGTCTCCCAATCAGATGAGC 845
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATGTAATTTGCAAGAAGACGAAG 840
|||
Db 846 ATGATGATTTGGCCAGAAATGAAGAAGTTTGAGATGTAATTTGCAAGAAGACGAAG 905
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTAATCCGGTTCTGACTTTT 900
|||
Db 906 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGTAATCCGGTTCTGACTTTT 965
QY 901 GAGAGGTGTTCATCATGATCAACAAGAACGGGCTCGTTTATCACAGTAGAGAG 960
|||
Db 966 GAGAGGTGTTCATCATGATCAACAAGAACGGGCTCGTTTATCACAGTAGAGAG 1025
QY 961 CAGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
|||
Db 1026 CAGAGCTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTGAAGAATTTGATTACG 1080
|||
Db 1086 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACCTGAAGAATTTGATTACG 1145
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1140
|||
Db 1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1205

QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 4

US-10-120-104

; Sequence 104, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinaiyan, Arul M.
; APPLICANT: Sreekumar, Arun
; APPLICANT: Rubin, Mark A.
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-104

Query Match 100.0%; Score 1146; DB 16; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

72000

QY 1 ATGGCACTGCAGGGCATCTCGGTGAGAGCTGTCCGGCCCGGGCCGTTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTGAGAGCTGTCCGGCCCGGGCCGTTCTGT 125
QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGCTGTGTGACGCGTGAACCGCCGCTCCGC 120
Db 126 GCTATGCTCTGGCTGACTTCGGGCGCGCTGTGTGACGCGTGAACCGCCGCTCCGC 185
QY 121 TACGACGTGAGCCGCTTGGGCGGGCAAGCGCTCGTAGTCTGGAACCTGAAGACCG 180
Db 186 TACGACGTGAGCCGCTTGGGCGGGCAAGCGCTCGTAGTCTGGAACCTGAAGACCG 245
QY 181 CGGGAGCCCGCGCTGCTGCGGCGTGTGCAAGCGGTCGATGTCTGCTGAGCCCTTC 240
Db 246 CGGGAGCCCGCGCTGCTGCGGCGTGTGCAAGCGGTCGATGTCTGCTGAGCCCTTC 305
QY 241 CGCCGCGGTGTCTATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
Db 306 CGCCGCGGTGTCTATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 365
QY 301 AGGCTATTATGAGCAGGCTGAGTGAATTGGCCAGTCAAGAACTTCTGCGGTTAGCT 360
Db 366 AGGCTATTATGAGCAGGCTGAGTGAATTGGCCAGTCAAGAACTTCTGCGGTTAGCT 425
QY 361 GGGCAGATATCAACTATTGGCTTGTCAAGTGTCTCTCAAAATGGCAGAAAGTGT 420
Db 426 GGGCAGATATCAACTATTGGCTTGTCAAGTGTCTCTCAAAATGGCAGAAAGTGT 485
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTGTGCTGCTGCTATGTGT 480
Db 486 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTGTGCTGCTGCTATGTGT 545
QY 481 GCACTGGGCAATTATATGCTCTTTTGAACCGACACGACACTGGCAGAGGTCAGTCAAT 540
Db 546 GCACTGGGCAATTATATGCTCTTTTGAACCGACACGACACTGGCAGAGGTCAGTCAAT 605
QY 541 GATGCAAAATATGCTGGAAGAACGATATTTAAGTCTTTCTGTGAAAACTCAGAAA 600
Db 606 GATGCAAAATATGCTGGAAGAACGATATTTAAGTCTTTCTGTGAAAACTCAGAAA 665

QY 601 TCGAGTCTGTGGGAAGCACTCCAGAGACAGAACATGTGGATGTGGAGCACCTTTCTAT 660
Db 666 TCGAGTCTGTGGGAAGCACTCCAGAGACAGAACATGTGGATGTGGAGCACCTTTCTAT 725
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTTTC 720
Db 726 ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTTTC 785
QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAAAGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAAAGAACGAAG 840
Db 846 ATGATGATTGGCCAGAAATGAAGAAGATTGGCAGATGTATTTGCAAAAGAACGAAG 905
QY 841 GCAGAGTGTGTCAAAATCTTTGACCGGACAGATGCTGTGTAATCCGTTCTGACTTTT 900
Db 906 GCAGAGTGTGTCAAAATCTTTGACCGGACAGATGCTGTGTAATCCGTTCTGACTTTT 965
QY 901 GAGGAGTGTGTCAATCATGATCAACAACAAGAACCGGGCTCGTTATCAACAGTGAAGAG 960
Db 966 GAGGAGTGTGTCAATCATGATCAACAACAAGAACCGGGCTCGTTATCAACAGTGAAGAG 1025
QY 961 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTAAACACCCAGCATCCCTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTAAACACCCAGCATCCCTCTTTC 1085
QY 1021 AAAAGGATCCTTTCAATGAGAAACACACTGAGAGATACTTGAAGAAATTTGATCAGC 1080
Db 1086 AAAAGGATCCTTTCAATGAGAAACACACTGAGAGATACTTGAAGAAATTTGATCAGC 1145
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAAAGTAAAGCT 1140
Db 1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAAAGTAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 5

US-10-909-035-104

; Sequence 104, Application US/10909035
; Publication No. US20050136493A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Mark A.
; APPLICANT: Chinaiyan, Arul M.
; APPLICANT: Lakshman, Bharathi
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: AMACR Cancer Markers
; FILE REFERENCE: UM-09098
; CURRENT APPLICATION NUMBER: US/10/909,035
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-909-035-104

Query Match 100.0%; Score 1146; DB 22; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCAATCTCGGTGAGAGCTGTCCGGCCCGGGCCGTTCTGT 60
Db 66 ATGGCACTGCAGGCAATCTCGGTGAGAGCTGTCCGGCCCGGGCCGTTCTGT 125
QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGTGACGCGTGAACCGGCGGCTCCGC 120
Db 126 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGTGACGCGTGAACCGGCGGCTCCGC 185

QY 121 TACGACGTGAGCCGCTTGGCCGGGCAAGCGCTCGTAGTGTGACTGAAGCAGCCG 180
DB 186 TACGACGTGAGCCGCTTGGCCGGGCAAGCGCTCGTAGTGTGACTGAAGCAGCCG 245
QY 181 CGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTCGGATGTGCTGTGAGCCCTTC 240
DB 246 CGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTCGGATGTGCTGTGAGCCCTTC 305
QY 241 CGCCCGGCTGTATGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 300
DB 306 CGCCCGGCTGTATGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 365
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
DB 366 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 425
QY 361 GGGCAGATATCAACTATTGCTTGTGAGTGTCTCTCAAAAAATTGGCAGAGTGTGT 420
DB 426 GGGCAGATATCAACTATTGCTTGTGAGTGTCTCTCAAAAAATTGGCAGAGTGTGT 485
QY 421 GAGATCCGATATGCCCCGCTGATCTCTGCTGACTTGTGCTGTGCTGCTTATGTGT 480
DB 486 GAGATCCGATATGCCCCGCTGATCTCTGCTGACTTGTGCTGTGCTGCTTATGTGT 545
QY 481 GCATGGGCAATTATATGCGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
DB 546 GCATGGGCAATTATATGCGCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 605
QY 541 GATGCAAAATATGCTGGAAGGAAGCAAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAA 600
DB 606 GATGCAAAATATGCTGGAAGGAAGCAAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAA 665
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGATGTTGAGCACTTTCTAT 660
DB 666 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGATGTTGAGCACTTTCTAT 725
QY 661 ACGACTTACAGACAGCAGATGGGGAATTATGCGCTGTTGAGCAATAGAACCCCAAGTTC 720
DB 726 ACGACTTACAGACAGCAGATGGGGAATTATGCGCTGTTGAGCAATAGAACCCCAAGTTC 785
QY 721 TACGAGCTGTGATCAAAAGCACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
DB 786 TACGAGCTGTGATCAAAAGCACTTGGACTTAAAGTCTGATGAATCTCCCAATCAGATGAGC 845
QY 781 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGAGATGTATTTGCAAAAGAACGAAAG 840
DB 846 ATGATGATTTGGCCAGAAATGAAGAAAGTTTGAGATGTATTTGCAAAAGAACGAAAG 905
QY 841 GCAGAGTGTGTCAAAATCTTTGACCGGACAGATGCTGTGATCTCGGTTCTGACTTTT 900
DB 906 GCAGAGTGTGTCAAAATCTTTGACCGGACAGATGCTGTGATCTCGGTTCTGACTTTT 965
QY 901 GAGAGGTTGTTTATCATGATCACAACAAGAAACGGGGCTCGTTATCAACCAAGTAGAG 960
DB 966 GAGAGGTTGTTTATCATGATCACAACAAGAAACGGGGCTCGTTATCAACCAAGTAGAG 1025
QY 961 CAGGACGTGAGCCCCCGCTGCACTGTGCTGTTAAACACCCCAAGCATCCCTTCTTTC 1020
DB 1026 CAGGACGTGAGCCCCCGCTGCACTGTGCTGTTAAACACCCCAAGCATCCCTTCTTTC 1085
QY 1021 AAAAGGATCTTTTATAGAGAAACAAGTGAAGATACCTTGAAGAAATTGGATTGAGC 1080
DB 1086 AAAAGGATCTTTTATAGAGAAACAAGTGAAGATACCTTGAAGAAATTGGATTGAGC 1145
QY 1081 CGCGAAGATTTATCAGCTTAATCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1140
DB 1146 CGCGAAGATTTATCAGCTTAATCAGATAAAATCATTGAAAGTAATAAGTAAAGCT 1205
QY 1141 AGTCTC 1146
DB 1206 AGTCTC 1211

RESULT 6
US-09-967-305-4
; Sequence 4, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Monahan, John
; APPLICANT: Richardson, Jennifer
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; PRIOR FILING DATE: 2001-09-28
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90) ... (1235)
US-09-967-305-4
Query Match 100.0%; Score 1146; DB 9; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTGTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 60
DB 90 ATGGCACTGCAGGGCATCTCGGTGTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 149
QY 61 GCTATGCTCTGCTGCTGACTTTCGGGCGCGTGTGTGACGCGTGAACCGGCGTCCGC 120
DB 150 GCTATGCTCTGCTGCTGACTTTCGGGCGCGTGTGTGACGCGTGAACCGGCGTCCGC 209
QY 121 TACGACGTGAGCCGCTTGGGCGGGAAGCGCTGCTAGTGTGAAAGCAGCCG 180
DB 210 TACGACGTGAGCCGCTTGGGCGGGAAGCGCTGCTAGTGTGAAAGCAGCCG 269
QY 181 CGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240
DB 270 CGGGAGCCCGCGTGTGCGGCGTGTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 329
QY 241 CGCCCGGCTGTATGAGAAATCTCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
DB 330 CGCCCGGCTGTATGAGAAATCTCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 389
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGTTAGCT 360
DB 390 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGTTAGCT 449
QY 361 GGGCAGATATCAACTATTGCTTGTGAGGTTCTCTCAAAAAATTGGCAGAAAGTGT 420
DB 450 GGGCAGATATCAACTATTGCTTGTGAGGTTCTCTCAAAAAATTGGCAGAAAGTGT 509
QY 421 GAGATCCGATATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTATGTGT 480
DB 510 GAGATCCGATATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGTGCTGTATGTGT 569
QY 481 GCATGGGCAATTATATGCTCTTTTGTACCGGACACGCACTGGCAAGGTCAGGTCAAT 540
DB 570 GCATGGGCAATTATATGCTCTTTTGTACCGGACACGCACTGGCAAGGTCAGGTCAAT 629
QY 541 GATGCAAAATATGTTGAAGGAACAAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAA 600
DB 630 GATGCAAAATATGTTGAAGGAACAAGCATATTTAAGTCTTTCTGTGAAAACTCAGAAA 689
QY 601 TCGAGTCTGTGGGAAGCACCTGAGAGACAGAACATGTTGATGTTGAGCACCTTTCTAT 660
DB 690 TCGAGTCTGTGGGAAGCACCTGAGAGACAGAACATGTTGATGTTGAGCACCTTTCTAT 749

QY 661 ACGACTTACAGACAGACAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCCACTTC 720
Db 750 ACGACTTACAGACAGACAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCCACTTC 809
QY 721 TACGAGCTGCTGATCAAAAGACTTGGAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGACTTGGAAGTCTGATGAATCTCCCAATCAGATGAGC 869
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCCAAGAAGACGAG 840
Db 870 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCCAAGAAGACGAG 929
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATCAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 960
Db 990 GAGGAGTGTTCATCATGATCAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 1049
QY 961 CAGGAGCTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db 1050 CAGGAGCTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1109
QY 1021 AAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAAGAATTTGGATTGAGC 1080
Db 1110 AAAAGGATCTTTCATAGAGAACACACTGAGAGATCTTGAAGAATTTGGATTGAGC 1169
QY 1081 CCGGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAAGTAAAGCT 1140
Db 1170 CCGGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAAGTAAAGTAAAGCT 1229
QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235

RESULT 7
US-10-205-823-17
; Sequence 17, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Gialt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17

LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-17

Query Match 100.0%; Score 1146; DB 15; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGGCATCTCGCTGAGAGCTGTCCGGCTGGCCCCGGCGTCTGT 60
Db 90 ATGGCACTGCAGGGGCATCTCGCTGAGAGCTGTCCGGCTGGCCCCGGCGTCTGT 149
QY 61 GCTATGCTCTGCTGACTTCGGGGCGCGGTGTGTAACCGGTGAGACCGGCCCTCCGC 120
Db 150 GCTATGCTCTGCTGACTTCGGGGCGCGGTGTGTAACCGGTGAGACCGGCCCTCCGC 209
QY 121 TACGACGTAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGACCTGAAGACGCCG 180
Db 210 TACGACGTAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGACCTGAAGACGCCG 269
QY 181 CCGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGATGTGCTGAGCCCTTC 240
Db 270 CCGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGATGTGCTGAGCCCTTC 329
QY 241 CCGCGCGGTGTATGAGAACTCCAGCTGGGCCCAAGATTCTGCAGCGGGAATCCA 300
Db 330 CCGCGCGGTGTATGAGAACTCCAGCTGGGCCCAAGATTCTGCAGCGGGAATCCA 389
QY 301 AGGCTTATTATGCCAGGCTGAGTGTGATTTGCCAGTCAAGAACTTCTGCCGTTAGCT 360
Db 390 AGGCTTATTATGCCAGGCTGAGTGTGATTTGCCAGTCAAGAACTTCTGCCGTTAGCT 449
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCAAAAATTGGCAGAGTGTGT 420
Db 450 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCAAAAATTGGCAGAGTGTGT 509
QY 421 GAGAAATCCGATATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGCTGATGTGT 480
Db 510 GAGAAATCCGATATGCCCCCGCTGAATCTCTGCTGACTTGTGCTGCTGATGTGT 569
QY 481 GCACTGGCATTTAATGGCTTTTGGACCGCACAGCACTGGCAAGGCTCAGTCAAT 540
Db 570 GCACTGGCATTTAATGGCTTTTGGACCGCACAGCACTGGCAAGGCTCAGTCAAT 629
QY 541 GATGCAATATGTGGAAGAACACAGCATATTTAGTCTTTTGTGGAATCTCAGAAA 600
Db 630 GATGCAATATGTGGAAGAACACAGCATATTTAGTCTTTTGTGGAATCTCAGAAA 689
QY 601 TCGAGTCTGTGGAGCACTCGAGACAGACATGTTGATGTTGAGCAGCACTTTCTAT 660
Db 690 TCGAGTCTGTGGAGCACTCGAGACAGACATGTTGATGTTGAGCAGCACTTTCTAT 749
QY 661 ACGACTTACAGACAGACAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCCACTTC 720
Db 750 ACGACTTACAGACAGACAGATGGGAATTTCATGGCTGTGGAGCAATAGAACCCCACTTC 809
QY 721 TACGAGCTGCTGATCAAAAGACTTGGAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGACTTGGAAGTCTGATGAATCTCCCAATCAGATGAGC 869
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCCAAGAAGACGAG 840
Db 870 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTAATTTGCCAAGAAGACGAG 929
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATCAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 960
Db 990 GAGGAGTGTTCATCATGATCAACAAGAACGGGCTGTTTATCACCAGTGAAGAG 1049

QY 961 CAGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCGACCCATCCCTTCTTTC 1020
 Db 1050 CAGACGTGAGCCCCCGCCCTGACCTCTGCTGTTAAACACCCGACCCATCCCTTCTTTC 1109
 QY 1021 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1080
 Db 1110 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1169
 QY 1081 CGCGAAGAGATTATCAGCTTAACCTGAGATAAATCATTTGAAGTTAAGTTAAAGCT 1140
 Db 1170 CGCGAAGAGATTATCAGCTTAACCTGAGATAAATCATTTGAAGTTAAGTTAAAGCT 1229
 QY 1141 AGTCTC 1146
 Db 1230 AGTCTC 1235

RESULT 8

US-09-967-305-6
 ; Sequence 6, Application US/09967305 ✓
 ; Patent No. US20020123081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Richardson, Jennifer
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-COA RACEMASE IN HORMONE
 ; FILE REFERENCE: 07334-312001
 ; CURRENT APPLICATION NUMBER: US/09/967,305
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: US 60/236,238
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 3654
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (90)....(1271)
 ; US-09-967-305-6

2

Query Match 98.8%; Score 1132; DB 9; Length 3654;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGACGGGATCTCGGTGGAAGCTGTCCGGCTGCGCCCGGCTTCTGT 60
 Db 90 ATGGCACTGACGGGATCTCGGTGGAAGCTGTCCGGCTGCGCCCGGCTTCTGT 149
 QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGGTGTGTACCGCTGACCGGCTCCGC 120
 Db 150 GCTATGCTCTGGCTGACTTCGGGCGCGGTGTGTGTACCGCTGACCGGCTCCGC 209
 QY 121 TACGACGTGAGCGGCTTGGGCGGCGCAAGCGCTGCTAGTCTGACCTGAAGCAGCG 180
 Db 210 TACGACGTGAGCGGCTTGGGCGGCGCAAGCGCTGCTAGTCTGACCTGAAGCAGCG 269
 QY 181 CGGGAGCCCGGCTGCTGCGGCTGTGTGCAAGCGGTGCTGCTGAGCCCTTC 240
 Db 270 CGGGAGCCCGGCTGCTGCGGCTGTGTGCAAGCGGTGCTGCTGAGCCCTTC 329
 QY 241 CGCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 300
 Db 330 CGCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGACGCGGAAATCCA 389
 QY 301 AGGCTATTATGCCAGGCTGAGATTGGCCAGTCAAGAACTTCTGCCGCTTACT 360
 Db 390 AGGCTATTATGCCAGGCTGAGATTGGCCAGTCAAGAACTTCTGCCGCTTACT 449
 QY 361 GGGCAGATATCAACTATTGGCTTGTGTCAGGTGTTCTCAAAAATTGGCAGAACTGCT 420
 Db 450 GGGCAGATATCAACTATTGGCTTGTGTCAGGTGTTCTCAAAAATTGGCAGAACTGCT 509

QY 421 GAGATCCGTATGCCCCCGCTGAAATCTCCTGGCTGACTTGTGCTGCTTATGTGT 480
 Db 510 GAGATCCGTATGCCCCCGCTGAAATCTCCTGGCTGACTTGTGCTGCTTATGTGT 569
 QY 481 GCATGGGCATTATATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGTCA 540
 Db 570 GCATGGGCATTATATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGTCA 629
 QY 541 GATGCAATATGTGGAAGAACACATATTAAAGTTCTTTCTGTGAAAACCTCAGAA 600
 Db 630 GATGCAATATGTGGAAGAACACATATTAAAGTTCTTTCTGTGAAAACCTCAGAA 689
 QY 601 TCGAGTCTGTGGAGACCTCTGAGAGACAGAACATGTTGATGTTGAGCACCCTTCTAT 660
 Db 690 TCGAGTCTGTGGAGACCTCTGAGAGACAGAACATGTTGATGTTGAGCACCCTTCTAT 749
 QY 661 ACAGCTTACAGACAGACAGATGGGGAATTTCATGCTGTTGAGCAATAGAACCCAGTTC 720
 Db 750 ACAGCTTACAGACAGACAGATGGGGAATTTCATGCTGTTGAGCAATAGAACCCAGTTC 809
 QY 721 TACGACGTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTCCCATCAGATGAGC 780
 Db 810 TACGACGTGCTGATCAAGAGACTTGGACTAAAGTCTGATGAATCTCCCATCAGATGAGC 869
 QY 781 ATGATGATTGGCCAGAAATGAAGAAAGTTTGACATGTAATTTGCAAGAAAGAGAG 840
 Db 870 ATGATGATTGGCCAGAAATGAAGAAAGTTTGACATGTAATTTGCAAGAAAGAGAG 929
 QY 841 GCAGAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGACTCCGTTCTGACTTTT 900
 Db 930 GCAGAGTGTGTCAAAATCTTTGACGCGCACAGATGCTGTGACTCCGTTCTGACTTTT 989
 QY 901 GAGAGGTTGTTTCATCATGATCAACAAGAAAGGCTGCTTATCACCAGTGAAGAG 960
 Db 990 GAGAGGTTGTTTCATCATGATCAACAAGAAAGGCTGCTTATCACCAGTGAAGAG 1049
 QY 961 CAGACGTGAGCCCCCGCCCTGCACTCTGCTGTAAACAACCCAGCATCCCTTCTTTC 1020
 Db 1050 CAGACGTGAGCCCCCGCCCTGCACTCTGCTGTAAACAACCCAGCATCCCTTCTTTC 1109
 QY 1021 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1080
 Db 1110 AAAAGGATCCTTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1169
 QY 1081 CGCGAAGAGATTATCAGCTTAACCTGAGATAAATCATTTGAAGTTAAGG 1132
 Db 1170 CGCGAAGAGATTATCAGCTTAACCTGAGATAAATCATTTGAAGTTAAGG 1221

RESULT 9

US-10-205-823-19
 ; Sequence 19, Application US/10205823
 ; Publication No. US20030108963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Ganavarapu, Manjula
 ; APPLICANT: Gorbacheva, Bella
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Kamakar, Shubhangi
 ; APPLICANT: Monsey, Angela M.
 ; APPLICANT: Glatz, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Anderson, Dustin
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MRI-044
 ; CURRENT APPLICATION NUMBER: US/10/205,823
 ; PRIOR FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/307,982

20-8-0

; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-19

Query Match 98.8%; Score 1132; DB 15; Length 3654;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCGATCTCGGTCTGGAGCTGTCCGGCTGCCCCGGCCGTTCTGT 60
Db ATGGCACTGCAGGCGATCTCGGTCTGGAGCTGTCCGGCTGCCCCGGCCGTTCTGT 149
QY 61 GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db GCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 209
QY 121 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGTCTGACCTGAAGCAGCCG 180
Db TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGCTAGTCTGACCTGAAGCAGCCG 269
QY 181 CCGGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db CCGGAGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329
QY 241 CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 300
Db CGCCGCGGTGTCATGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 389
QY 301 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGTTAGCT 360
Db AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGTTAGCT 449
QY 361 GGGCAGCATATCACTATTGGCTTGTCTGAGGTGTTCTCTCAAAATTGGCAGAAAGTGT 420
Db GGGCAGCATATCACTATTGGCTTGTCTGAGGTGTTCTCTCAAAATTGGCAGAAAGTGT 509
QY 421 GAGAAATCCGTATGCCCCGCTGAATCTCTGGCTGACTTGTGCTGCTGCTGCTGCTGCTGCT 480
Db GAGAAATCCGTATGCCCCGCTGAATCTCTGGCTGACTTGTGCTGCTGCTGCTGCTGCTGCT 569
QY 481 GCACTGGGCATTATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGTCAAT 540
Db GCACTGGGCATTATATGCTCTTTTGAACCGCACACGCACTGGCAAGGTCAGTCAAT 629
QY 541 GATGCAATATATGTTGGAAGAACAGCATATTTAAGTTCTTTCTGTGAAACTCAGAAA 600
Db GATGCAATATATGTTGGAAGAACAGCATATTTAAGTTCTTTCTGTGAAACTCAGAAA 689
QY 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGTTGAGCACTTTCTAT 660
Db TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGATGTTGAGCACTTTCTAT 749
QY 661 ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTTC 720
Db ACGACTTACAGGACAGAGATGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTTC 809
QY 721 TAGGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db TAGGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCTCCCAATCAGATGAGC 869

QY 781 ATGATGATTGGCCAGAAATGAAGAAGAGTTCAGATGTATTTCGAAGAAGACGAAG 840
Db ATGATGATTGGCCAGAAATGAAGAAGAGTTCAGATGTATTTCGAAGAAGACGAAG 929
QY 841 GCAGAGTGTGTCAATCTTTTGAACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db GCAGAGTGTGTCAATCTTTTGAACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATCACAACAAGGAACGGGCTGTTATCACCAGTGAGGAG 960
Db GAGGAGTGTTCATCATGATCACAACAAGGAACGGGCTGTTATCACCAGTGAGGAG 1049
QY 961 CAGGACGTGAGCCCCCGCTGCACTCTGCTTTAAACACCCAGCCATCCCTTCTTTC 1020
Db CAGGACGTGAGCCCCCGCTGCACTCTGCTTTAAACACCCAGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGAATTGGATTGAGC 1080
Db AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGAATTGGATTGAGC 1169
QY 1110 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATACTTGAAGAATTGGATTGAGC 1169
Db 1170 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAAG 1221

RESULT 10

US-10-205-823-25
; Sequence 25, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-25

7820

Query Match 95.5%; Score 1095; DB 15; Length 2069;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCGATCTCGGTCTGGAGCTGTCCGGCTGCCCCGGCCGTTCTGT 60
Db ATGGCACTGCAGGCGATCTCGGTCTGGAGCTGTCCGGCTGCCCCGGCCGTTCTGT 149

QY 61 GCTATGCTCTGCTGACTTCGGGGCGGTGTGTACGCGTGACCGGCGGCTCCCGC 120
Db 150 GCTATGCTCTGCTGACTTCGGGGCGGTGTGTACGCGTGACCGGCGGCTCCCGC 209
QY 121 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 269
QY 181 CGGGAGCCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGCTGCTGAGCCCTTC 240
Db 270 CGGGAGCCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGCTGCTGAGCCCTTC 329
QY 241 CGCCGCGGTGTATGAGAACTCCAGCTGGCCAGAGATTCTGACGGGAAATCCA 300
Db 330 CGCCGCGGTGTATGAGAACTCCAGCTGGCCAGAGATTCTGACGGGAAATCCA 389
QY 301 AGGCTTATTATGACGCTGAGTGAATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
Db 390 AGGCTTATTATGACGCTGAGTGAATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 449
QY 361 GGCCACGATATCACTATTGGCTTTGTGAGGTGTCTCTCAAAATTTGGCAGAGTGT 420
Db 450 GGCCACGATATCACTATTGGCTTTGTGAGGTGTCTCTCAAAATTTGGCAGAGTGT 509
QY 421 GAGATCCGTATGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 510 GAGATCCGTATGCCCGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
QY 481 GCACTGGGCAATTATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAAGTCA 540
Db 570 GCACTGGGCAATTATATGCTCTTTTGAACCGCACAGCACTGGCAAGGTCAAGTCA 629
QY 541 GATGCAATATATGTGAGAGAACACATATTTAAGTCTTTCTGTGAAAATCTCAGAA 600
Db 630 GATGCAATATATGTGAGAGAACACATATTTAAGTCTTTCTGTGAAAATCTCAGAA 689
QY 601 TCGAGTCTGTGGAGACACCTCGAGACAGAAATGTTGATGTTGAGCACTTTCTAT 660
Db 690 TCGAGTCTGTGGAGACACCTCGAGACAGAAATGTTGATGTTGAGCACTTTCTAT 749
QY 661 ACGACTTACAGACAGACAGATGGGAATTCATGCTGTGAGCAATAGAACCCCACTTC 720
Db 750 ACGACTTACAGACAGACAGATGGGAATTCATGCTGTGAGCAATAGAACCCCACTTC 809
QY 721 TACGAGCTGCTGATCAAAAGACTTGAATTAAGTCTGATGAATTTCCCAATCAGATGAC 780
Db 810 TACGAGCTGCTGATCAAAAGACTTGAATTAAGTCTGATGAATTTCCCAATCAGATGAC 869
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAAAGAACAGAG 840
Db 870 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAAAGAACAGAG 929
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGATCTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGATCTCCGGTTCTGACTTTT 989
QY 901 GAGGAGTGTGTATCATGATCAACAAGAAAGGGCTGTTTATCACCAGTGAAGAG 960
Db 990 GAGGAGTGTGTATCATGATCAACAAGAAAGGGCTGTTTATCACCAGTGAAGAG 1049
QY 961 CAGGACGTGAGCCCGCGCTGCACTCTGCTTAAACACCCCAAGCATCCCTTTTTC 1020
Db 1050 CAGGACGTGAGCCCGCGCTGCACTCTGCTTAAACACCCCAAGCATCCCTTTTTC 1109
QY 1021 AAAAGGATCTTTATAGAGAACACACTGAGAGATATCTGAAGAATTTGATTCAGC 1080
Db 1110 AAAAGGATCTTTATAGAGAACACACTGAGAGATATCTGAAGAATTTGATTCAGC 1169
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCATTGAAAGTAAAGTAAAGCT 1140
Db 1170 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCATTGAAAGTAAAGTAAAGCT 1229
QY 1141 AGTCTC 1146

Db 1230 AGTCTC 1235
RESULT 11
US-10-205-823-27
; Sequence 27, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-205-823-27
Query Match 94.3%; Score 1081; DB 15; Length 2626;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCACTGACGGGCACTCTCGGTGAGCTGTCCGGCTGCCCCGGCGGCTTCTGT 60
Db 90 ATGGCACTGACGGGCACTCTCGGTGAGCTGTCCGGCTGCCCCGGCGGCTTCTGT 149
QY 61 GCTATGCTCTGCTGACTTCGGGGCGGTGTGTAAGCGGTGACCGGCGGCTCCCGC 120
Db 150 GCTATGCTCTGCTGACTTCGGGGCGGTGTGTAAGCGGTGACCGGCGGCTCCCGC 209
QY 121 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCGCTTGGGCGGCGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 269
QY 181 CGGGAGCCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGCTGCTGAGCCCTTC 240
Db 270 CGGGAGCCGCGCTGCTGCGGCGCTGTGCAAGCGGTGCGATGCTGCTGAGCCCTTC 329
QY 241 CGCCGCGGTGTATGAGAACTCCAGCTGGCCAGAGATTCTGACGGGAAATCCA 300
Db 330 CGCCGCGGTGTATGAGAACTCCAGCTGGCCAGAGATTCTGACGGGAAATCCA 389
QY 301 AGGCTTATTATGACGCTGAGTGAATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360
Db 390 AGGCTTATTATGACGCTGAGTGAATTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 449
QY 361 GGCCACGATATCACTATTGGCTTTGTGAGGTGTCTCTCAAAATTTGGCAGAGTGT 420

Db 450 GGGCCAGATATCAACTATTTGGCTTTGTGAGGTGTTCTTCAAAAATTGGCAGAGTGGT 509
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGGTGGTGGCTTATGT 480
Db 510 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGGTGGTGGCTTATGT 569
QY 481 GCACTGGGCATTATATGCTCTTTTGGACCGCACCGACTGGCAAGGTCAGTCAAT 540
Db 570 GCACTGGGCATTATATGCTCTTTTGGACCGCACCGACTGGCAAGGTCAGTCAAT 629
QY 541 GATGCAATATGTTGGAGAGAACACATATTTAAGTCTTTCTGTGAAAATCTCAGAA 600
Db 630 GATGCAATATGTTGGAGAGAACACATATTTAAGTCTTTCTGTGAAAATCTCAGAA 689
QY 601 TCGAGTCTGTGGAGACACCTCGAGAGACAGAACATGTTGGATGGTGGACACCTTTAT 660
Db 690 TCGAGTCTGTGGAGACACCTCGAGAGACAGAACATGTTGGATGGTGGACACCTTTAT 749
QY 661 ACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACATAGAACCCCACTTC 720
Db 750 ACGACTTACAGACAGACAGATGGGAATTCATGCTGTTGGACATAGAACCCCACTTC 809
QY 721 TACGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGACTTGAATAAGTCTGATGAATCCCAATCAGATGAGC 869
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 840
Db 870 ATGATGATTTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 929
QY 841 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 930 GCAGAGTGTGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 989
QY 901 GAGAGGTGTTTCATCATGATCAACAAGAACGGGCTCTTTATCACCAGTGAAGAG 960
Db 990 GAGAGGTGTTTCATCATGATCAACAAGAACGGGCTCTTTATCACCAGTGAAGAG 1049
QY 961 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTCTTTC 1020
Db 1050 CAGGACGTGAGCCCCCGCTGCACTCTGCTGTTAAACACCCAGCCATCCCTCTTTC 1109
QY 1021 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1080
Db 1110 AAAAGGATCCTTTCATAGAGAACACACTGAGAGATCTTGAAGATTGGATTGAGC 1169
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAGTAATAAGG 1132
Db 1170 CGCGAAGAGATTATCAGCTTAACTCAGATAAATCATTTGAAGTAATAAGG 1221

RESULT 12

US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

6/10

; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107

Query Match 93.4%; Score 1070; DB 9; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGTCTATGCTCCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCTGGCCCCGGCCGCTTCTGTCTATGCTCCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGTACCGCGTGAACCGGCGGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 145
Db 90 CGCGTGTGTACCGCGTGAACCGGCGGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 149
QY 146 GCAAGCGCTCGCTAGTGTGGAAGCTGAAGCAGCCGCGGAGCCGCGTGTGCGGCTC 205
Db 150 GCAAGCGCTCGCTAGTGTGGAAGCTGAAGCAGCCGCGGAGCCGCGTGTGCGGCTC 209
QY 206 TGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTCGCGCGGTGTCATGAGAACTCC 265
Db 210 TGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTCGCGCGGTGTCATGAGAACTCC 269
QY 266 AGCTGGGCCCCAGAGATCTGACAGCGGGAATCCAGGCTTATTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCCCAGAGATCTGACAGCGGGAATCCAGGCTTATTATGCCAGGCTGAGTG 329
QY 326 GATTTGGCCAGTCAAGAACTTCTGCGGTTAGTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTTGGCCAGTCAAGAACTTCTGCGGTTAGTGGCCACGATATCAACTATTGGCTT 389
QY 386 TGTCAAGTGTCTCTCAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 445
Db 390 TGTCAAGTGTCTCTCAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTGTGCTGTGAGAACTCAGAAATCGAGTCTGTGGAGACACTCGAG 505
Db 450 TCCTGGCTGACTTGTGCTGTGAGAACTCAGAAATCGAGTCTGTGGAGACACTCGAG 509
QY 506 TTGACCGCACACGCACTGGCAAGGTCAGGTCATGATGCAAAATATGTTGGAAGAACAG 565
Db 510 TTGACCGCACACGCACTGGCAAGGTCAGGTCATGATGCAAAATATGTTGGAAGAACAG 569
QY 566 CATATTTAAGTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAGACACTCGAG 625
Db 570 CATATTTAAGTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAGACACTCGAG 629
QY 626 GACAGAACATGTTGATGTTGAGACACCTTTCTATAGCACTTACAGAGACAGATGGGG 685
Db 630 GACAGAACATGTTGATGTTGAGACACCTTTCTATAGCACTTACAGAGACAGATGGGG 689
QY 686 AATTCATGCTGTGTGAGCAATAGAACCCCACTTCAAGCTGTGATCAAGGAAGCTTG 745
Db 690 AATTCATGCTGTGTGAGCAATAGAACCCCACTTCAAGCTGTGATCAAGGAAGCTTG 749
QY 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGAGATGTATTTGCAAGAAGACGAAGCAGAGTGTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGAGATGTATTTGCAAGAAGACGAAGCAGAGTGTGTCAAAATCTTTGACG 869

QY 866 GCACAGATGCTGTGTACTCCGGTTCTGACTTTTGAGAGGTTGTCATCATGATCACA 925
DB 870 GCACAGATGCTGTGTACTCCGGTTCTGACTTTTGAGAGGTTGTCATCATGATCACA 929
QY 926 ACAAGAACCGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGACCCCGCTGCAC 985
DB 930 ACAAGAACCGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGACCCCGCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCCGCATCCCTTTCTTCAAAAGGATCCTTCATAGAGAAC 1045
DB 990 CTCTGCTGTTAAACACCCCGCATCCCTTTCTTCAAAAGGATCCTTCATAGAGAAC 1049
QY 1046 ACACGTGAGAGATCTTGAAGATTGGATTGACCGCGAAGAGATTATCAGCTTAAC 1105
DB 1050 ACACGTGAGAGATCTTGAAGATTGGATTGACCGCGAAGAGATTATCAGCTTAAC 1109
QY 1106 CAGATAAATCATTTGAAGTAATAAGCTAGTCTC 1146
DB 1110 CAGATAAATCATTTGAAGTAATAAGCTAGTCTC 1150

RESULT 13

US-09-780-669-107
; Sequence 107, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-107

Query Match 93.4%; Score 1070; DB 9; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCGGGCTGGCCCGGCGTCTGTGTATGTCCTGCTGACTTGGGG 85
DB 30 TGGAGCTGTCGGGCTGGCCCGGCGTCTGTGTATGTCCTGCTGACTTGGGG 89
QY 86 CGCGTGTGTAACGCGTGACCGGCGGCTCCGCTACGACGTAGCCGCTTGGCGGG 145
DB 90 CGCGTGTGTAACGCGTGACCGGCGGCTCCGCTACGACGTAGCCGCTTGGCGGG 149
QY 146 GCAAGCGCTCGTAGTGTGACCTGAAGCAAGCGGCGGAGCGCGCTGCTGCGGCTC 205

DB 150 GCACGCTCGCTAGTGTGACCTGAAGCAGCCGCGGAGACCCGCTGCTGCGGCTC 209
QY 206 TGTGCAAGCGGCTCGGATGTGCTGTGAGCCCTTCCGCGCGGTGTCTATGAGAACTCC 265
DB 210 TGTGCAAGCGGCTCGGATGTGCTGTGAGCCCTTCCGCGCGGTGTCTATGAGAACTCC 269
QY 266 AGCTGGGCCCCAGAGATTCTGACCGGGAATAATCCAAGGCTTATTATGCCAGGCTGAGTG 325
DB 270 AGCTGGGCCCCAGAGATTCTGACCGGGAATAATCCAAGGCTTATTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAAGAGCTTCTGCGGTTAGCTGGCCAGATATCAACTATTGGCTT 385
DB 330 GATTGGCCAGTCAAGAGCTTCTGCGGTTAGCTGGCCAGATATCAACTATTGGCTT 389
QY 386 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGAGTGAGAAATCCGTATGCCCGCTGATC 445
DB 390 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGAGTGAGAAATCCGTATGCCCGCTGATC 449
QY 446 TCTGCTGCTGACTTGTGCTGCTGCTGCTTATGTGTGCTGCTGCTGCTTATATGCTCTTT 505
DB 450 TCTGCTGCTGACTTGTGCTGCTGCTGCTTATGTGTGCTGCTGCTGCTTATATGCTCTTT 509
QY 506 TTGACCGCACACGACCTGGCAGAGGTCAGGTCAATGATGCAATATGTGGAAGAAACAG 565
DB 510 TTGACCGCACACGACCTGGCAGAGGTCAGGTCAATGATGCAATATGTGGAAGAAACAG 569
QY 566 CATATTTAGTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAAGCACTGAG 625
DB 570 CATATTTAGTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGAAGCACTGAG 629
QY 626 GACAGAACATGTTGATGTGAGACACCTTCTATACACTTACAGACAGACAGATGGGG 685
DB 630 GACAGAACATGTTGATGTGAGACACCTTCTATACACTTACAGACAGACAGATGGGG 689
QY 686 AATTCATGCTGTGAGCAATAGAACCCAGTCTTACAGACTGCTGATCAAAAGACTTG 745
DB 690 AATTCATGCTGTGAGCAATAGAACCCAGTCTTACAGACTGCTGATCAAAAGACTTG 749
QY 746 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAGA 805
DB 750 GACTAAAGTCTGATGAATCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAGA 809
QY 806 AGAGTTTGACAGATGATTTGCAAGAGAGAGAGAGAGAGAGTGTGCAATCTTTGACG 865
DB 810 AGAGTTTGACAGATGATTTGCAAGAGAGAGAGAGAGAGAGTGTGCAATCTTTGACG 869
QY 866 GCACAGATGCTGTGTACTCCGTTCTGACTTTTGAGAGCTTGTTCATCATGATCACA 925
DB 870 GCACAGATGCTGTGTACTCCGTTCTGACTTTTGAGAGCTTGTTCATCATGATCACA 929
QY 926 ACAAGAACCGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGACCCCGCTGCAC 985
DB 930 ACAAGAACCGGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGACCCCGCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCCGCATCCCTTTCTTCAAAAGGATCCTTCATAGAGAAC 1045
DB 990 CTCTGCTGTTAAACACCCCGCATCCCTTTCTTCAAAAGGATCCTTCATAGAGAAC 1049
QY 1046 ACACGTGAGAGATCTTGAAGATTGGATTGACCGCGAAGAGATTATCAGCTTAAC 1105
DB 1050 ACACGTGAGAGATCTTGAAGATTGGATTGACCGCGAAGAGATTATCAGCTTAAC 1109
QY 1106 CAGATAAATCATTTGAAGTAATAAGCTAGTCTC 1146
DB 1110 CAGATAAATCATTTGAAGTAATAAGCTAGTCTC 1150

RESULT 14

US-09-030-606-107
; Sequence 107, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-107

Query Match 93.4%; Score 1070; DB 9; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCCTGGCCCCCGCGTCTGTGCTATGCTCTGGCTGACTTCGGGG 85
DB 30 TGGAGCTGTCCGGCCTGGCCCCCGCGTCTGTGCTATGCTCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGTACGCGGTGACCGCGCGCGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 145
DB 90 CGCGTGTGTACGCGGTGACCGCGCGCGCTCCCGCTACGACGTGAGCCGCTTGGCGGG 149
QY 146 GCAAGCGCTCGCTAGTGTGCTGACCTGAAGCAGCCGCGGGAGCCGCGCTGCGCGCTC 205
DB 150 GCAAGCGCTCGCTAGTGTGCTGACCTGAAGCAGCCGCGGGAGCCGCGCTGCGCGCTC 209
QY 206 TGTGCAAGCGGTCGGATGTGCTGCTGAGACCCCTTCCGCGCGGCTCATGAGAACTCC 265
DB 210 TGTGCAAGCGGTCGGATGTGCTGCTGAGACCCCTTCCGCGCGGCTCATGAGAACTCC 269
QY 266 AGCTGGGCCCCAGAGATTCTGACGCGGAAAAATCCAAAGGCTTATTATGCCAGGCTGAGTG 325
DB 270 AGCTGGGCCCCAGAGATTCTGACGCGGAAAAATCCAAAGGCTTATTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAGGAAGCTTCTGCGCGTTAGCTGGCCACGATATCAACTATTGGCTT 385
DB 330 GATTGGCCAGTCAGGAAGCTTCTGCGCGTTAGCTGGCCACGATATCAACTATTGGCTT 389
QY 386 TGTCAAGTGTCTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 445
DB 390 TGTCAAGTGTCTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTGCTGTGTGCTGCTTATGTGTGCACTGGGCAATTAAATGAGCTCTT 505
DB 450 TCCTGGCTGACTTTGCTGTGTGCTGCTTATGTGTGCACTGGGCAATTAAATGAGCTCTT 509

QY 506 TTGACCGCACACGCACTGGCAAGGCTCAGTCAATGATGCAATATGTGAGGAACAG 565
DB 510 TTGACCGCACACGCACTGCAAGGCTCAGTCAATGATGCAATATGTGAGGAACAG 569
QY 566 CATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAAGCACTCGAG 625
DB 570 CATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAAGCACTCGAG 629
QY 626 GACAGAACATGTTGATGCTGAGACCACTTCTATACGACTTACAGACAGACGATGGGG 685
DB 630 GACAGAACATGTTGATGCTGAGACCACTTCTATACGACTTACAGACAGACGATGGGG 689
QY 686 AATTCATGGCTGTTGAGCAATAGAACCCCACTTCAAGAGCTGCTGATCAAGAGACTTG 745
DB 690 AATTCATGGCTGTTGAGCAATAGAACCCCACTTCAAGAGCTGCTGATCAAGAGACTTG 749
QY 746 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805
DB 750 GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGACAGATGTAATTGCAAGAAGACGAGGAGTGTGTCAAATCTTGACG 865
DB 810 AGAAGTTTGACAGATGTAATTGCAAGAAGACGAGGAGTGTGTCAAATCTTGACG 869
QY 866 GCACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGAGAGTGTTCATCATGATCACA 925
DB 870 GCACAGATGCTGTGTGACTCCGGTCTGACTTTTGAGAGAGTGTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAGAGACGACGTGAGCCCCCGCTGCAC 985
DB 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAGAGACGACGTGAGCCCCCGCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTCAAAAGGATCCTTTCATAGAGAAC 1045
DB 990 CTCTGCTGTTAAACACCCCAAGCCATCCCTTCTTCAAAAGGATCCTTTCATAGAGAAC 1049
QY 1046 ACACTGAGAGATACCTGAAGATTGGATTACGCCGGAAGATTATCAGCTTAACT 1105
DB 1050 ACACTGAGAGATACCTGAAGATTGGATTACGCCGGAAGATTATCAGCTTAACT 1109
QY 1106 CAGATAAATCATTTGAAGTAATAAGTAAAGCTAGTCTC 1146
DB 1110 CAGATAAATCATTTGAAGTAATAAGTAAAGCTAGTCTC 1150

RESULT 15

US-09-822-827-107
; Sequence 107, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-107

Query Match 93.4%; Score 1070; DB 9; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCCTGGCCCCCGCGTCTGTGCTATGCTCTGGCTGACTTCGGGG 85
DB 30 TGGAGCTGTCCGGCCTGGCCCCCGCGTCTGTGCTATGCTCTGGCTGACTTCGGGG 89

QY 86 CGCGTGTGTACCGCTGGACCGGCCCCGCTCCCGCTACGACGTGAGCCGCTTGGGCCCCG 145
 DB 90 CGCGTGTGTACCGCTGGACCGGCCCCGCTCCCGCTACGACGTGAGCCGCTTGGGCCCCG 149
 QY 146 GCAAGCGCTCGTAGTGTGTGACCTGAAGCAGCCGCGGGAGCCCGCTGTGCGCGCTC 205
 DB 150 GCAAGCGCTCGTAGTGTGTGACCTGAAGCAGCCGCGGGAGCCCGCTGTGCGCGCTC 209
 QY 206 TGTGCAAGCGGTGCGATGTGTGTGAGCCCTTCCCGCGGTGTCAAGAACTCC 265
 DB 210 TGTGCAAGCGGTGCGATGTGTGTGAGCCCTTCCCGCGGTGTCAAGAACTCC 269
 QY 266 AGCTGGGCCAGAGATTCTGACGCGGAAATCCAAGGCTTATTATGCCAGGCTGAGTG 325
 DB 270 AGCTGGGCCAGAGATTCTGACGCGGAAATCCAAGGCTTATTATGCCAGGCTGAGTG 329
 QY 326 GATTGGCCAGTCAGGAAGCTTCTGCGGTTAGCTGGCCAGATATCACTATTGGCTT 385
 DB 330 GATTGGCCAGTCAGGAAGCTTCTGCGGTTAGCTGGCCAGATATCACTATTGGCTT 389
 QY 386 TGTCAAGTGTCTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 445
 DB 390 TGTCAAGTGTCTCTCAAAAATTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 449
 QY 446 TCCTGGCTGACTTTGCTGTGTGTGCTTATGTGTGCACTGGGCAATTAATGGCTCTT 505
 DB 450 TCCTGGCTGACTTTGCTGTGTGTGCTTATGTGTGCACTGGGCAATTAATGGCTCTT 509
 QY 506 TTGACCGCACACGCACTGGCAAGGCTCAGGTCAATTGATGCAAAATATGTGGAAGAACAG 565
 DB 510 TTGACCGCACACGCACTGGCAAGGCTCAGGTCAATTGATGCAAAATATGTGGAAGAACAG 569
 QY 566 CATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAGACACCTCGAG 625
 DB 570 CATATTTAAGTCTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGAGACACCTCGAG 629
 QY 626 GACAGAACATGTGTGATGTGTGAGCACTTTCTATACGACTTACAGACAGCAGATGGGG 685
 DB 630 GACAGAACATGTGTGATGTGTGAGCACTTTCTATACGACTTACAGACAGCAGATGGGG 689
 QY 686 AATTCATGGCTGTGTGAGCAATAGAACCCCGCTTCTACGAGCTGCTGATCAAGGACTTG 745
 DB 690 AATTCATGGCTGTGTGAGCAATAGAACCCCGCTTCTACGAGCTGCTGATCAAGGACTTG 749
 QY 746 GACTAAAGTCTGTATGAATCTTCCCAATCAGATGACATGATGATTTGGCCAGAAATGAAGA 805
 DB 750 GACTAAAGTCTGTATGAATCTTCCCAATCAGATGACATGATGATTTGGCCAGAAATGAAGA 809
 QY 806 AGAAGTTTGCAAGTGTATTTGCAAAAGAGCAGAGGCGAGTGTGCAATCTTTGACG 865
 DB 810 AGAAGTTTGCAAGTGTATTTGCAAAAGAGCAGAGGCGAGTGTGCAATCTTTGACG 869
 QY 866 GCACAGATGCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTCATCATGATCACA 925
 DB 870 GCACAGATGCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTCATCATGATCACA 929
 QY 926 ACAAGGACGGGCTCGTTTATCACAGTGAGAGCAGAGCAGAGCTGAGCCCGCCCTGCAC 985
 DB 930 ACAAGGACGGGCTCGTTTATCACAGTGAGAGCAGAGCAGAGCTGAGCCCGCCCTGCAC 989
 QY 986 CTCTGCTGTAAACACCCAGCCATCCCTTCTTCAAAAAGGATCCTTTCATAGAGAAC 1045
 DB 990 CTCTGCTGTAAACACCCAGCCATCCCTTCTTCAAAAAGGATCCTTTCATAGAGAAC 1049
 QY 1046 ACACTGAGAGATACTGAAGAATTGTGATTCAGCCGGAAGAGATTATCAGCTTAACT 1105
 DB 1050 ACACTGAGAGATACTGAAGAATTGTGATTCAGCCGGAAGAGATTATCAGCTTAACT 1109
 QY 1106 CAGATAAATCATTTGAAGTAATAAGTAAGCTAGTCTC 1146
 DB 1110 CAGATAAATCATTTGAAGTAATAAGTAAGCTAGTCTC 1150

Search completed: July 27, 2005, 12:53:49
 Job time : 845 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 05:32:03 ; Search time 230 Seconds
(without alignments)
8152.927 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagtagtctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1142.8	99.7	1621	3	US-09-020-956-107 Sequence 107, App
2	1142.8	99.7	1621	3	US-09-030-607-107 Sequence 107, App
3	1142.8	99.7	1621	3	US-09-439-313-107 Sequence 107, App
4	1142.8	99.7	1621	3	US-09-352-616A-107 Sequence 107, App
5	1142.8	99.7	1621	3	US-09-232-149A-107 Sequence 107, App
6	1142.8	99.7	1621	4	US-09-159-812-107 Sequence 107, App
7	1142.8	99.7	1621	4	US-09-636-215-107 Sequence 107, App
8	1142.8	99.7	1621	4	US-09-685-166A-107 Sequence 107, App
9	1142.8	99.7	1621	4	US-09-115-453-107 Sequence 107, App
10	1142.8	99.7	1621	4	US-09-688-489-107 Sequence 107, App
11	1142.8	99.7	1621	4	US-09-679-426-107 Sequence 107, App
12	1142.8	99.7	1621	4	US-09-759-143-107 Sequence 107, App
13	1142.8	99.7	1621	4	US-09-651-236-107 Sequence 107, App
14	428.4	37.4	430	4	US-09-702-705-1504 Sequence 1504, Ap
15	428.4	37.4	430	4	US-09-736-457-1504 Sequence 1504, Ap
16	428.4	37.4	430	4	US-09-614-124B-1504 Sequence 1504, Ap
17	428.4	37.4	430	4	US-09-671-325-1504 Sequence 1504, Ap
18	428.4	37.4	430	4	US-09-658-824-1504 Sequence 1504, Ap
C 19	406.6	35.5	773	3	US-09-020-956-3 Sequence 3, Appli
C 20	406.6	35.5	773	3	US-09-030-607-3 Sequence 3, Appli
C 21	406.6	35.5	773	3	US-09-439-313-3 Sequence 3, Appli
C 22	406.6	35.5	773	3	US-09-352-616A-3 Sequence 3, Appli
C 23	406.6	35.5	773	3	US-09-232-149A-3 Sequence 3, Appli
C 24	406.6	35.5	773	4	US-09-159-812-3 Sequence 3, Appli
C 25	406.6	35.5	773	4	US-09-636-215-3 Sequence 3, Appli
C 26	406.6	35.5	773	4	US-09-685-166A-3 Sequence 3, Appli
C 27	406.6	35.5	773	4	US-09-115-453-3 Sequence 3, Appli

C 28	406.6	35.5	773	4	US-09-688-489-3	Sequence 3, Appli
C 29	406.6	35.5	773	4	US-09-679-426-3	Sequence 3, Appli
C 30	406.6	35.5	773	4	US-09-759-143-3	Sequence 3, Appli
C 31	406.6	35.5	773	4	US-09-651-236-3	Sequence 3, Appli
32	403.2	35.2	793	3	US-09-020-956-33	Sequence 33, Appl
33	403.2	35.2	793	3	US-09-030-607-33	Sequence 33, Appl
34	403.2	35.2	793	3	US-09-439-313-33	Sequence 33, Appl
35	403.2	35.2	793	3	US-09-352-616A-33	Sequence 33, Appl
36	403.2	35.2	793	3	US-09-232-149A-33	Sequence 33, Appl
37	403.2	35.2	793	4	US-09-159-812-33	Sequence 33, Appl
38	403.2	35.2	793	4	US-09-636-215-33	Sequence 33, Appl
39	403.2	35.2	793	4	US-09-685-166A-33	Sequence 33, Appl
40	403.2	35.2	793	4	US-09-115-453-33	Sequence 33, Appl
41	403.2	35.2	793	4	US-09-688-489-33	Sequence 33, Appl
42	403.2	35.2	793	4	US-09-679-426-33	Sequence 33, Appl
43	403.2	35.2	793	4	US-09-759-143-33	Sequence 33, Appl
44	403.2	35.2	793	4	US-09-651-236-33	Sequence 33, Appl
45	400.2	34.9	816	3	US-09-020-956-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-020-956-107
; Sequence 107, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCACTGCAGGGCATCTCGTGGAGCTGTCCGGCTGGCCCCCGGGCCGTTCTGT 60
|||||
Db 5 ATGGCACTGCAGGGCATCTCGTGGAGCTGTCCGGCTGGCCCCCGGGCCGTTCTGT 64

QY 61 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCCCGGCTCCCGC 120
Db |||||||
65 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCCCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 180
Db |||||||
125 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCGCGTGTCTGCGGCTGTGTGCAAGCGGTGCGATGTCTGTGGAGCCCTTC 240
Db |||||||
185 CGGGAGCCGCGTGTCTGCGGCTGTGTGCAAGCGGTGCGATGTCTGTGGAGCCCTTC 244

QY 241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||||
245 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 304

QY 301 AGGCTATTATGCCAGGCTAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db |||||||
305 AGGCTATTATGCCAGGCTAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364

QY 361 GGCCAGGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAAATTGGCAGAAGTGGT 420
Db |||||||
365 GGCCAGGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAAATTGGCAGAAGTGGT 424

QY 421 GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGTGGCTTATGTGT 480
Db |||||||
425 GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGTGGCTTATGTGT 484

QY 481 GCACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACTGGCAAGGTCAGGTCATT 540
Db |||||||
485 GCACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACTGACAAGGTCAGGTCATT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAAAACTCAGAAA 600
Db |||||||
545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGACACCTTTCTAT 660
Db |||||||
605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGACACCTTTCTAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCAATTC 720
Db |||||||
665 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCCAATTC 724

QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db |||||||
725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGCAAG 840
Db |||||||
785 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGCAAG 844

QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db |||||||
845 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904

QY 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db |||||||
905 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964

QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db |||||||
965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024

QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1080
Db |||||||
1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAAGGTAAGAGCT 1140
Db |||||||
1085 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAGTAATAAGGTAAGAGCT 1144

QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 2
US-09-030-607-107
; Sequence 107, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGCTGGCCCCGGGCCCGTTCTGT 60
Db |||||||
5 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGCTGGCCCCGGGCCCGTTCTGT 64

QY 61 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 120
Db |||||||
65 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG 180
Db |||||||
125 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCCGCGTGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTCTGTGGAGCCCTTC 240
Db |||||||
185 CGGGAGCCCGCGTGTCTGCGGCGTCTGTGCAAGCGGTGCGATGTCTGTGGAGCCCTTC 244

QY 241 CGCCCGCGGTGTATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||||
245 CGCCCGCGGTGTATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 304

QY 301 AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360

||||| 305 AGGCTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
Qy 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db 365 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGT 424
Qy 421 GAGAAATCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 480
Db 425 GAGAAATCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 484
Qy 481 GCACCTGGCATTTAATAGGCTCTTTTGGCCGACACGCTGGCAAGGTCAGTCAAT 540
Db 485 GCACCTGGCATTTAATAGGCTCTTTTGGCCGACACGCTGGCAAGGTCAGTCAAT 544
Qy 541 GATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTTGTGGAAACTCAGAAA 600
Db 545 GATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTTGTGGAAACTCAGAAA 604
Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 664
Qy 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 784
Qy 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGGAAG 840
Db 785 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGGAAG 844
Qy 841 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTAATCTCGGTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTAATCTCGGTTCTGACTTTT 904
Qy 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
Qy 961 CAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 965 CAGGAGCTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024
Qy 1021 AAAAGGATCCTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTGAGC 1080
Db 1025 AAAAGGATCCTTTATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTGAGC 1084
Qy 1081 CGGAAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAGCT 1140
Db 1085 CGGAAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAGCT 1144
Qy 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 3
US-09-439-313-107
; Sequence 107, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCTGGCCCCCGGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCTGGCCCCCGGCTTCTGT 64
Qy 61 GCTATGGTCTGTGGTACTTCCGGGGCGGTGTGGTACGGCTGGACCGGGCCGGCTCCGC 120
Db 65 GCTATGGTCTGTGGTACTTCCGGGGCGGTGTGGTACGGCTGGACCGGGCCGGCTCCGC 124
Qy 121 TACGACGTGAGCCGCTTGGCCGGGGCAAGCGCTCGTACTGTGACCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGGCCGGGGCAAGCGCTCGTACTGTGACCTGAAGCAGCCG 184
Qy 181 CGGGGAGCCCGCTGTCTGGCGCTCTGTCAAGCGCTCGGATGTCTGTGGAGCCCTTC 240
Db 185 CGGGGAGCCCGCTGTCTGGCGCTCTGTCAAGCGCTCGGATGTCTGTGGAGCCCTTC 244
Qy 241 CGCCCGGCTGTCTATGGAGAACTCCAGCTGGGGCCAGAGATTTGCAGCGGGAAATCCA 300
Db 245 CGCCCGGCTGTCTATGGAGAACTCCAGCTGGGGCCAGAGATTTGCAGCGGGAAATCCA 304
Qy 301 AGGCTTATTTATGCCAGGTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 305 AGGCTTATTTATGCCAGGTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364
Qy 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db 365 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGT 424
Qy 421 GAGAAATCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 480
Db 425 GAGAAATCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGTGGCTTATGTT 484
Qy 481 GCACCTGGCATTTAATAGGCTCTTTTGAACCGCACACGCTGGCAAGGTCAGGTCAAT 540
Db 485 GCACCTGGCATTTAATAGGCTCTTTTGAACCGCACACGCTGGCAAGGTCAGGTCAAT 544
Qy 541 GATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTTGTGGAAACTCAGAAA 600
Db 545 GATGCAATATGTTGGAAGGAACAGCATATTTAAGTCTTTTGTGGAAACTCAGAAA 604
Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 664
Qy 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATCTCCCAATCAGATGAGC 784
Qy 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGGAAG 840

Db 785 ATGATGATTGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAGACGAAG 844
Qy 841 GCAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904
Qy 901 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTATCACCAGTGAGGAG 964
Qy 961 CAGGAGTGAGCCCCCGCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
Db 965 CAGGAGTGAGCCCCCGCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1024
Qy 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1080
Db 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1084
Qy 1081 CGGAAGAGATTTATCAGCTTAAGTAACTCAGATAAAATCATTGAAAGTAAAGCT 1140
Db 1085 CGGAAGAGATTTATCAGCTTAAGTAACTCAGATAAAATCATTGAAAGTAAAGCT 1144
Qy 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 4

US-09-352-616A-107
; Sequence 107, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-107

Query Match 99.7%; Score 1142.8; DB 3; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCCCTGGCCCCCGGCTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCCCTGGCCCCCGGCTTCTGT 64
Qy 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGACCGCGCCCGGCTCCCGC 120
Db 65 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGACCGCGCCCGGCTCCCGC 124
Qy 121 TACGACGTGAGCCCGCTTGGGCCGGGCAACGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCCGCTTGGGCCGGGCAACGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 184
Qy 181 CGGGAGCCCGCGTGTGCGGCGCTGTGCAAGCGGTCCGATGTCTGCTGGAGCCCTTC 240
Db 185 CGGGAGCCCGCGTGTGCGGCGCTGTGCAAGCGGTCCGATGTCTGCTGGAGCCCTTC 244
Qy 241 CGCCGGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCAGCGGGGAAATCCA 300

Db 245 CGCCCGGTGTCTATGGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 304
Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTCTGCCGTTAGCT 364
Qy 361 GGCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 420
Db 365 GGCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 424
Qy 421 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 484
Qy 481 GCACCTGGGCATTATAATGGCTCTTTTGTAGCCGCACACGCACTGGCAAGGTCAGTCAAT 540
Db 485 GCACCTGGGCATTATAATGGCTCTTTTGTAGCCGCACACGCACTGCAAGGGTCAGTCAAT 544
Qy 541 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGAAGAAACAGCATATTTAAGTCTTTTCTGTGAAAACTCAGAAA 604
Qy 601 TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGAGCACCTTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGAGCACCTTTCTAT 664
Qy 661 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGTTTC 720
Db 665 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGTTTC 724
Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784
Qy 781 ATGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAGAACGAAAG 840
Db 785 ATGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAGAACGAAAG 844
Qy 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904
Qy 901 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
Qy 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTGTTAAACACCCCGCATCCCTTCTTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTGTTAAACACCCCGCATCCCTTCTTTC 1024
Qy 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1080
Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1084
Qy 1081 CGGAAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAAGCT 1140
Db 1085 CGGAAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAAAGCT 1144
Qy 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 5

US-09-232-149A-107
; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

Db 365 GGCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT 424

Qy 421 GAGATCCGTATGCCCCGCTGAATCTCTGGCTGACTTTTGGTGGTGGTGGCTTATGTGT 480

Db 425 GAGATCCGTATGCCCCGCTGAATCTCTGGCTGACTTTTGGTGGTGGTGGCTTATGTGT 484

Qy 481 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGGTCAGGTCAATT 540

Db 485 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACACGCACTGACAAGGGTCAGGTCAATT 544

Qy 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 604

Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 664

Qy 661 ACGACTTACAGGACAGCAGATGGGAATTATGCTGTTGGAGCAATAGAACCCCAAGTTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGAATTATGCTGTTGGAGCAATAGAACCCCAAGTTC 724

Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784

Qy 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 840

Db 785 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 844

Qy 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900

Db 845 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904

Qy 901 GAGGAGTGTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960

Db 905 GAGGAGTGTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964

Qy 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020

Db 965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024

Qy 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1080

Db 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1084

Qy 1081 CGCGAAGAGATTTATCAGCTTAACACAGATAAAATCATTTGAAGTAATAAGGTAAAGCT 1140

Db 1085 CGCGAAGAGATTTATCAGCTTAACACAGATAAAATCATTTGAAGTAATAAGGTAAAGCT 1144

Qy 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 7
US-09-636-215-107

; Sequence 107, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGCCCTGGCCCCGGCCCGTTCGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTCTATGGAGCTGTCGGCCCTGGCCCCGGCCCGTTCGT 64

Qy 61 GCTATGGTCTTGGTGAATTCGGGGCGCGTGTGTACCGCTGGACCGCGCCGGTCCCGC 120

Db 65 GCTATGGTCTTGGTGAATTCGGGGCGCGTGTGTACCGCTGGACCGCGCCGGTCCCGC 124

Qy 121 TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGTCTCGTAGTCTGGACCTGAAGCAGCG 180

Db 125 TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGTCTCGTAGTCTGGACCTGAAGCAGCG 184

Qy 181 CGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCCCTTC 240

Db 185 CGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGTGGAGCCCTTC 244

Qy 241 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGGCCAGAGATTCTGCAGCGGGAATCCA 300

Db 245 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGGCCAGAGATTCTGCAGCGGGAATCCA 304

Qy 301 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360

Db 305 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 364

Qy 361 GGCCACGATATCAACTATTTGGCTTTGTAGGTGTTCTCTCAAAAATTGGCAGAAAGTGT 420

Db 365 GGCCACGATATCAACTATTTGGCTTTGTAGGTGTTCTCTCAAAAATTGGCAGAAAGTGT 424

Qy 421 GAGAACTCCGTATGCCCCGCTGAATCTCTGGTGAATTTGGTGGTGGTGGTGGTGGTGGT 480

Db 425 GAGAACTCCGTATGCCCCGCTGAATCTCTGGTGAATTTGGTGGTGGTGGTGGTGGTGGT 484

Qy 481 GCAGTGGGCATTATAATGCTCTTTTGACCCGCACACGCACTGGCAAGGGTCAGGTCAATT 540

Db 485 GCAGTGGGCATTATAATGCTCTTTTGACCCGCACACGCACTGACAAGGGTCAGGTCAATT 544

Qy 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 604

Qy 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 664

Qy 661 ACGACTTACAGGACAGCAGATGGGAATTATGCTGTTGGAGCAATAGAACCCCAAGTTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGAATTATGCTGTTGGAGCAATAGAACCCCAAGTTC 724

Qy 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAAAGAACGACGAAG 840
Db 785 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTGCAAAAGAACGACGAAG 844
QY 841 GCAGAGTGGTCAAAATCTTTGACGSCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTCAAAATCTTTGACGSCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCCTTCTTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCCTTCTTTC 1024
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1080
Db 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1140
Db 1085 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 8

US-09-685-166A-107

; Sequence 107, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

- ; APPLICANT: Xu, Jiangchun
- ; APPLICANT: Dillon, Davin C.
- ; APPLICANT: Mitcham, Jennifer L.
- ; APPLICANT: Harlocker, Susan L.
- ; APPLICANT: Jiang, Yuqui
- ; APPLICANT: Henderson, Robert A.
- ; APPLICANT: Kalos, Michael D.
- ; APPLICANT: Fanger, Gary R.
- ; APPLICANT: Retter, Marc W.
- ; APPLICANT: Stolk, John A.
- ; APPLICANT: Day, Craig H.
- ; APPLICANT: Vedvick, Thomas S.
- ; APPLICANT: Carter, Darrick
- ; APPLICANT: Li, Samuel
- ; APPLICANT: Wang, Aijun
- ; APPLICANT: Skeiky, Yasir A.W.
- ; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-685-166A-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTGCTGAGAGCTGTCCGGCCCTGGCCCGGGCCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTGCTGAGAGCTGTCCGGCCCTGGCCCGGGCCCGTTCTGT 64

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCGCGCTCCCGC 120

Db 65 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGGTGGACCGGCGCGCTCCCGC 124
QY 121 TAGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCGG 180
Db 125 TAGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCGG 184
QY 181 CGGGAGCCGCGTGTGTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGAGCCGCGTGTGTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 244
QY 241 CGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATCCA 300
Db 245 CGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATCCA 304
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 364
QY 361 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 365 GGCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAATTTGGCAGAAAGTGGT 424
QY 421 GAGAATCCGTATGCCCCGCTGAATCTCTGGCTGACTTTTGTGTTGGTGGCTTATGTGT 480
Db 425 GAGAATCCGTATGCCCCGCTGAATCTCTGGCTGACTTTTGTGTTGGTGGCTTATGTGT 484
QY 481 GCAGTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCATT 540
Db 485 GCAGTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCATT 544
QY 541 GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTGTGGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTGTGGAAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTTCTAT 720
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTTCTAT 724
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTCTAT 720
Db 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTCTAT 724
QY 721 TAGGAGTCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 725 TAGGAGTCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784
QY 781 ATGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAAGAACGAAAG 840
Db 785 ATGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAAGAACGAAAG 844
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCCCTGACACCTCTGCTGTAAACACCCAGCCATCCCCTTCTTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCCTGACACCTCTGCTGTAAACACCCAGCCATCCCCTTCTTTC 1024
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1080
Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1084
QY 1081 CGGAAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1140
Db 1085 CGGAAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 9

US-09-115-453-107

; Sequence 107, Application US/09115453B

; Patent No. 6657056

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

; TITLE OF INVENTION: METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C4

; CURRENT APPLICATION NUMBER: US/09/115,453B

; CURRENT FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-115-453-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 64

QY 61 GCTATGTCCTGGTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGGCTCCCGC 120

Db 65 GCTATGTCCTGGTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180

Db 125 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCGCGTGTGCGGGCGTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240

Db 185 CGGGAGCCGCGTGTGCGGGCGTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 244

QY 241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 300

Db 245 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 360

Db 305 AGGCTTATTTATGCCAGGCTGAGTGATTTGGCCAGTCAAGAGCTTCTGCCGTTAGCT 364

QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420

Db 365 GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 424

QY 421 GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 480

Db 425 GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 484

QY 481 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGGTCAGGTCAAT 540

Db 485 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGGTCAGGTCAAT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTCTGTGGAACCTCAGAAA 604

QY 601 TCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660

Db 605 TCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 664

QY 661 ACGACTTACAGACAGCAGATGGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720

Db 665 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAAGGACTTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAAGGACTTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTATTTGCAAAGAAGACGAAG 840

Db 785 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTATTTGCAAAGAAGACGAAG 844

QY 841 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900

Db 845 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 904

QY 901 GAGGAGTGTTCATCATGATCAACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960

Db 905 GAGGAGTGTTCATCATGATCAACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964

QY 961 CAGGACGTGAGCCCCCGCTTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020

Db 965 CAGGACGTGAGCCCCCGCTTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024

QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTCAGC 1080

Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTCAGC 1084

QY 1081 CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAAGCT 1140

Db 1085 CGCGAAGAGATTTTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAAGCT 1144

QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 10

US-09-688-489-107

; Sequence 107, Application US/09688489

; Patent No. 6664377

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427D2

; CURRENT APPLICATION NUMBER: US/09/688,489

; CURRENT FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-688-489-107

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTCTGAGAGCTGTCCGGCTGGCCCCCGGCGTCTGT 64

QY 61 GCTATGTCCTGGTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGGCTCCCGC 120

Db 65 GCTATGTCCTGGTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180

Db 125 TACGACGTGAGCCGCTTGGGGCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCGCGTGTGCGGGCGTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240

```
Db 185 CCGGGAGCCGCGTGTGGCGGTCTGTGCAAGCGTCCGATGTGCTGGAGCCCTTC 244
QY 241 CGCCGCGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAGAAATCCA 300
Db 245 CGCCGCGGTGTATGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAGAAATCCA 304
QY 301 AGGCTTATTATGCGAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTTATTATGCGAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATGGCAGAAGTGGT 420
Db 365 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATGGCAGAAGTGGT 424
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 484
QY 481 GCACTGGGCATTATTAATGGCTCTTTTGGACCGCACGCACTGGCAAGGTCAGGTCATT 540
Db 485 GCACTGGGCATTATTAATGGCTCTTTTGGACCGCACGCACTGACAAGGTCAGGTCATT 544
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTTCTAT 660
Db 605 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAACTGTTGGATGGTGGAGCACTTTCTAT 664
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGTGATCAAAAGCACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 784
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGATTTGCAAGAAGACGAAG 840
Db 785 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACAGATGATTTGCAAGAAGACGAAG 844
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 965 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1080
Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1084
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGTAAAGCT 1144
QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150
```

RESULT 11

US-09-679-426-107

; Sequence 107, Application US/09679426

; Patent No. 6759515

; GENERAL INFORMATION:

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-107
```

Query Match 99.7%; Score 1142.8; DB 4; Length 1621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCCGGCCCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCATGAGAGCTGTCCGGCCTGGCCCCCGGCCCCGTTCTGT 64
QY 61 GCTATGTCCTGGCTGACTTCCGGGCGCGTGTGGTACGCGTGACCGGCCCGGCTCCCGC 120
Db 65 GCTATGTCCTGGCTGACTTCCGGGCGCGTGTGGTACGCGTGACCGGCCCGGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGCCGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGGCCGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 184
QY 181 CGGGAGCGCGCTGCTGCGGCGCTCTGTGCAAGCGTGTGCGATGTGCTGGAGCCCTTC 240
Db 185 CGGGAGCGCGCTGCTGCGGCGCTCTGTGCAAGCGTGTGCGATGTGCTGGAGCCCTTC 244
QY 241 CGCCGCGGTGTATGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 300
Db 245 CGCCGCGGTGTATGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 304
QY 301 AGGCTTATTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 305 AGGCTTATTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAAGTGGT 420
Db 365 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAATTTGGCAGAAGTGGT 424
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 484
QY 481 GCACTGGGCATTATTAATGGCTCTTTTGGACCGCACGCACTGGCAAGGTCAGGTCATT 540
Db 485 GCACTGGGCATTATTAATGGCTCTTTTGGACCGCACGCACTGACAAGGTCAGGTCATT 544
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 604
```


QY 601 TCGAGTCTGTGGGAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db |||||
QY 605 TCGAGTCTGTGGGAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 664
Db |||||
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db |||||
QY 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
Db |||||
QY 721 TACGAGTCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db |||||
QY 725 TACGAGTCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784
Db |||||
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAGAAGACGAAG 840
Db |||||
QY 785 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAGAAGACGAAG 844
Db |||||
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 900
Db |||||
QY 845 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 904
Db |||||
QY 901 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db |||||
QY 905 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
Db |||||
QY 961 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCCTTC 1020
Db |||||
QY 965 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCCTTC 1024
Db |||||
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTCAGC 1080
Db |||||
QY 1025 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTCAGC 1084
Db |||||
QY 1081 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1140
Db |||||
QY 1085 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAAAGCT 1144
Db |||||
QY 1141 AGTCTC 1146
Db |||||
QY 1145 AGTCTC 1150
Db |||||

RESULT 12

US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621

; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107
Query Match 99.7%; Score 1142.8; DB 4; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCCGGCTTCGT 60
Db |||||
QY 5 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCCGGCTTCGT 64
Db |||||
QY 61 GCTATGGTCTGTGGTACTTCGGGGCGCGTGTGTGTAACGCTGGACCGGCCCGGCTCCCGC 120
Db |||||
QY 65 GCTATGGTCTGTGGTACTTCGGGGCGCGTGTGTGTAACGCTGGACCGGCCCGGCTCCCGC 124
Db |||||
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 180
Db |||||
QY 125 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 184
Db |||||
QY 181 CGGGAGCCCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240
Db |||||
QY 185 CGGGAGCCCGCTGCTGCGCGCTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 244
Db |||||
QY 241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||
QY 245 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 304
Db |||||
QY 301 AGGCTATTATGCCAGGTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360
Db |||||
QY 305 AGGCTATTATGCCAGGTGAGTGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 364
Db |||||
QY 361 GGCCACGATATCAACTATTGGCTTTGT CAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGT 420
Db |||||
QY 365 GGCCACGATATCAACTATTGGCTTTGT CAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGT 424
Db |||||
QY 421 GAGAACTCCGTATGCCCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTT 480
Db |||||
QY 425 GAGAACTCCGTATGCCCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTT 484
Db |||||
QY 481 GCACCTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGSCAAGGGTCAGGTCAAT 540
Db |||||
QY 485 GCACCTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGSCAAGGGTCAGGTCAAT 544
Db |||||
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
Db |||||
QY 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 604
Db |||||
QY 601 TCGAGTCTGTGGGAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db |||||
QY 605 TCGAGTCTGTGGGAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 664
Db |||||
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db |||||
QY 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
Db |||||
QY 721 TACGAGTCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db |||||
QY 725 TACGAGTCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784
Db |||||
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAGAAGACGAAG 840
Db |||||
QY 785 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTAATTTGCAAGAAGACGAAG 844
Db |||||
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 900
Db |||||
QY 845 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 904
Db |||||
QY 901 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db |||||
QY 905 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
Db |||||
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCCTTC 1020
Db |||||

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1504
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1504

Query Match 37.4%; Score 428.4; DB 4; Length 430;
Best Local Similarity 99.8%; Pred. No. 1.5e-122;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 363 CCACGATATCAACTATTGGCTTTGTGTCAGGTGTTCTCTCAAAAAATTGGCAGAAAGTGGTGA 422
Db 1 CCACGATATCAACTATTGGCTTTGTGTCAGGTGTTCTCTCAAAAAATTGGCAGAAAGTGGTGA 60

QY 423 GAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTC 482
Db 61 GAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTC 120

QY 483 ACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGGTCAGGTCAATTGA 542
Db 121 ACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGGTCAGGTCAATTGA 180

QY 543 TGCAAAATATGGTGGAAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATC 602
Db 181 TGCAAAATATGGTGGAAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATT 240

QY 603 GAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTATAC 662
Db 241 GAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTATAC 300

QY 663 GACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTA 722
Db 301 GACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTA 360

QY 723 CGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCAT 782
Db 361 CGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCAT 420

QY 783 GGATGATTGG 792
Db 421 GGATGATTGG 430

RESULT 15
US-09-736-457-1504
; Sequence 1504, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457

; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1504
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1504

Query Match 37.4%; Score 428.4; DB 4; Length 430;
Best Local Similarity 99.8%; Pred. No. 1.5e-122;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 363 CCACGATATCAACTATTGGCTTTGTGTCAGGTGTTCTCTCAAAAAATTGGCAGAAAGTGGTGA 422
Db 1 CCACGATATCAACTATTGGCTTTGTGTCAGGTGTTCTCTCAAAAAATTGGCAGAAAGTGGTGA 60

QY 423 GAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTC 482
Db 61 GAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTC 120

QY 483 ACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGGTCAGGTCAATTGA 542
Db 121 ACTGGGCATTATAATGGCTCTTTTGTACCCGCACACGCACCTGGCAAGGGTCAGGTCAATTGA 180

QY 543 TGCAAAATATGGTGGAAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATC 602
Db 181 TGCAAAATATGGTGGAAAGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATT 240

QY 603 GAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTATAC 662
Db 241 GAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTATAC 300

QY 663 GACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTA 722
Db 301 GACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTA 360

QY 723 CGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCAT 782
Db 361 CGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCAT 420

QY 783 GGATGATTGG 792
Db 421 GGATGATTGG 430

Search completed: July 27, 2005, 09:01:51
Job time : 234 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 08:58:05 ; Search time 231 Seconds
(without alignments)
8117.633 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagtagtctc 1146

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1070	93.4	1621	3	US-09-020-956-107	Sequence 107, App
2	1070	93.4	1621	3	US-09-030-607-107	Sequence 107, App
3	1070	93.4	1621	3	US-09-439-313-107	Sequence 107, App
4	1070	93.4	1621	3	US-09-352-616A-107	Sequence 107, App
5	1070	93.4	1621	3	US-09-232-149A-107	Sequence 107, App
6	1070	93.4	1621	4	US-09-159-812-107	Sequence 107, App
7	1070	93.4	1621	4	US-09-636-215-107	Sequence 107, App
8	1070	93.4	1621	4	US-09-685-166A-107	Sequence 107, App
9	1070	93.4	1621	4	US-09-115-453-107	Sequence 107, App
10	1070	93.4	1621	4	US-09-688-489-107	Sequence 107, App
11	1070	93.4	1621	4	US-09-679-426-107	Sequence 107, App
12	1070	93.4	1621	4	US-09-759-143-107	Sequence 107, App
13	1070	93.4	1621	4	US-09-651-236-107	Sequence 107, App
14	398	34.7	816	3	US-09-020-956-2	Sequence 2, Appli
15	398	34.7	816	3	US-09-030-607-2	Sequence 2, Appli
16	398	34.7	816	3	US-09-439-313-2	Sequence 2, Appli
17	398	34.7	816	3	US-09-352-616A-2	Sequence 2, Appli
18	398	34.7	816	3	US-09-232-149A-2	Sequence 2, Appli
19	398	34.7	816	4	US-09-159-812-2	Sequence 2, Appli
20	398	34.7	816	4	US-09-636-215-2	Sequence 2, Appli
21	398	34.7	816	4	US-09-685-166A-2	Sequence 2, Appli
22	398	34.7	816	4	US-09-115-453-2	Sequence 2, Appli
23	398	34.7	816	4	US-09-688-489-2	Sequence 2, Appli
24	398	34.7	816	4	US-09-679-426-2	Sequence 2, Appli
25	398	34.7	816	4	US-09-759-143-2	Sequence 2, Appli
26	398	34.7	816	4	US-09-651-236-2	Sequence 2, Appli
27	379	33.1	430	4	US-09-702-705-1504	Sequence 1504, Ap

28	379	33.1	430	4	US-09-736-457-1504	Sequence 1504, Ap
29	379	33.1	430	4	US-09-614-124B-1504	Sequence 1504, Ap
30	379	33.1	430	4	US-09-671-325-1504	Sequence 1504, Ap
31	379	33.1	430	4	US-09-658-824-1504	Sequence 1504, Ap
32	314	27.4	386	4	US-09-513-999C-3525	Sequence 3525, Ap
33	305	26.6	773	3	US-09-020-956-3	Sequence 3, Appli
34	305	26.6	773	3	US-09-030-607-3	Sequence 3, Appli
35	305	26.6	773	3	US-09-439-313-3	Sequence 3, Appli
36	305	26.6	773	3	US-09-352-616A-3	Sequence 3, Appli
37	305	26.6	773	3	US-09-232-149A-3	Sequence 3, Appli
38	305	26.6	773	4	US-09-159-812-3	Sequence 3, Appli
39	305	26.6	773	4	US-09-636-215-3	Sequence 3, Appli
40	305	26.6	773	4	US-09-685-166A-3	Sequence 3, Appli
41	305	26.6	773	4	US-09-115-453-3	Sequence 3, Appli
42	305	26.6	773	4	US-09-688-489-3	Sequence 3, Appli
43	305	26.6	773	4	US-09-679-426-3	Sequence 3, Appli
44	305	26.6	773	4	US-09-759-143-3	Sequence 3, Appli
45	305	26.6	773	4	US-09-651-236-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-020-956-107
; Sequence 107, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-09-020-956-107
Query Match 93.4%; Score 1070; DB 3; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 TGGAGCTGTCCGGCCTGGCCCCGGCCCGTCTGTGCTATGGTCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCCGGCCCGTCTGTGCTATGGTCTGGCTGACTTCGGGG 89

|||||
Db 390 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 449
Qy 446 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGCACCTGGGCATTATAATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGCACCTGGGCATTATAATGGCTCTTT 509
Qy 506 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 565
Db 510 TTGACCGCACACGCACCTGACAAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 569
Qy 566 CATATTTAAAGTTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db 570 CATATTTAAAGTTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629
Qy 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689
Qy 686 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG 745
Db 690 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG 749
Qy 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 809
Qy 806 AGAAGTTTGCAGATGTAATTTGCAAAAGAAAGACGAGCGAGAGTGGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTAATTTGCAAAAGAAAGACGAGCGAGAGTGGTCAAAATCTTTGACG 869
Qy 866 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 929
Qy 926 ACAAGGAACGGGGCTCGTTTATCACCAAGTGGAGGACGAGCGTGGAGCGCCCGCTGACAC 985
Db 930 ACAAGGAACGGGGCTCGTTTATCACCAAGTGGAGGACGAGCGTGGAGCGCCCGCTGACAC 989
Qy 986 CTCTGCTGTTAAACACCCCGCATCCCTTCTTTCAAAAGGGATCCTTTATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCCGCATCCCTTCTTTCAAAAGGGATCCTTTATAGGAGAAC 1049
Qy 1046 AACTGAGGAGATACCTTGAAGAATTTGGATTGAGCGCGGAAGAGATTTATCAGCTTAACT 1105
Db 1050 AACTGAGGAGATACCTTGAAGAATTTGGATTGAGCGCGGAAGAGATTTATCAGCTTAACT 1109
Qy 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 3
US-09-439-313-107
; Sequence 107, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107

Query Match 93.4%; Score 1070; DB 3; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 TGGAGCTGTCCGGCTTGGCCCGGGCCCGGCTCTGTGTATGGTCTCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCTTGGCCCGGGCCCGGCTCTGTGTATGGTCTCTGGCTGACTTCGGGG 89
Qy 86 CGCGTGTGGTACCGCTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG 145
Db 90 CGCGTGTGGTACCGCTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG 149
Qy 146 GCAAGCGCTCGTAGTGTGTGGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGCGCGCTC 205
Db 150 GCAAGCGCTCGTAGTGTGTGGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGCGCGCTC 209
Qy 206 TGTCAAGCGGTGCGATGTGTGTGGAGCCCTTCCCGCGGGTGTCTATGGAGAAACTCC 265
Db 210 TGTCAAGCGGTGCGATGTGTGTGGAGCCCTTCCCGCGGGTGTCTATGGAGAAACTCC 269
Qy 266 AGCTGGGCCCAGAGATTCTGAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCCAGAGATTCTGAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329
Qy 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 389
Qy 386 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 449
Qy 446 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGACCTGGGCATTATAATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGACCTGGGCATTATAATGGCTCTTT 509
Qy 506 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 565
Db 510 TTGACCGCACACGCACCTGACAAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 569
Qy 566 CATATTTAAAGTTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db 570 CATATTTAAAGTTCTTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629
Qy 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689
Qy 686 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG 745
Db 690 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG 749
Qy 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 809
Qy 806 AGAAGTTTGCAGATGTAATTTGCAAAAGAAAGACGAGCGAGTGGTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTAATTTGCAAAAGAAAGACGAGCGAGTGGTGTCAAAATCTTTGACG 869
Qy 866 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 929
Qy 926 ACAAGGAACGGGGCTCGTTTATCACCAAGTGGAGGACGAGCGTGGAGCGCCCGCTGACAC 985

Db 930 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAAC 1049
QY 1046 ACACTGAGGAGATACATTGAAGAATTTGGATTACGCCGGAAGAGATTTATCAGCTTAACT 1105
Db 1050 ACACTGAGGAGATACATTGAAGAATTTGGATTACGCCGGAAGAGATTTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 4
US-09-352-616A-107
; Sequence 107, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-107

Query Match 93.4%; Score 1070; DB 3; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGGCCTGGCCCGGGCCCCGTTCTGTGTATGGTCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCGGGCCCCGTTCTGTGTATGGTCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGGTACGCGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTGCTGCGGCGTC 205
Db 90 CGCGTGTGGTACGCGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTGCTGCGGCGTC 209
QY 146 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTGCTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTGCTGCGGCGTC 209
QY 206 TGTGCAAGCGGTCCGATGTGCTGGAGCCCTTCCGCCCGGGTGTGCTATGGAGAACTCC 265
Db 210 TGTGCAAGCGGTCCGATGTGCTGGAGCCCTTCCGCCCGGGTGTGCTATGGAGAACTCC 269
QY 266 AGCTGGGCCCAGAGATTTGCGAGCGGGAATCCAAAGCTTATTTATGCCAGCTGAGTG 325
Db 270 AGCTGGGCCCAGAGATTTGCGAGCGGGAATCCAAAGCTTATTTATGCCAGCTGAGTG 329
QY 326 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTT 385
Db 330 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTT 389
QY 386 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGTGAGAAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATATGCTCTTTT 505

Db 450 TCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 509
QY 506 TTGACCGCACAGCACTGGCAAGGGTCAGGTCATTGATGCAAATATGTGGAAGGAACAG 565
Db 510 TTGACCGCACAGCACTGACNAGGGTCAGGTCATTGATGCAAATATGTGGAAGGAACAG 569
QY 566 CATATTTAAGTTCCTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db 570 CATATTTAAGTTCCTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 685
Db 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 689
QY 686 AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAAAGGACTTG 745
Db 690 AATTCATGGCTGTTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAAAGGACTTG 749
QY 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGTTGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGTTGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGTATTGTCAAAGAACAGGAGGAGGAGTGGTGTCAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTATTGTCAAAGAACAGGAGGAGGAGTGGTGTCAAATCTTTGACG 869
QY 866 GCACAGATGCCCTGTGTGACTCCGGTCTGACTTTTGGAGGTTTGTTCATCATGATCACA 925
Db 870 GCACAGATGCCCTGTGTGACTCCGGTCTGACTTTTGGAGGTTTGTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGAGGAGCGTGAGCCCCCGCCCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGAGGAGCGTGAGCCCCCGCCCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAAC 1049
QY 1046 ACACTGAGGAGATACTTGAAGAAATTTGGATTGAGCTTTCAGCCGCGAAGAGATTTATCAGCTTAACT 1105
Db 1050 ACACTGAGGAGATACTTGAAGAAATTTGGATTGAGCTTTCAGCCGCGAAGAGATTTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 5
US-09-232-149A-107
; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-107

Query Match 93.4%; Score 1070; DB 3; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGGCCTGGCCCGGGCCCCGTTCTGTGTATGGTCTGCTGACTTGGG 85

Db 30 TGGAGCTGTCCGGCCTGGCCCCGGGCCCGTTCTGTGCTATGGTCCTGGCTGACTTCGGGG 89
QY
Db 86 CGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGCGG 145
Db 90 CGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGCGG 149
QY 146 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGCGGCGTC 209
QY 206 TGTGCAAGCGGTCCGATGTGCTGGAGCCCTCCCGCGCGGTGTCTGCGGAACTCC 265
Db 210 TGTGCAAGCGGTCCGATGTGCTGGAGCCCTCCCGCGCGGTGTCTGCGGAACTCC 269
QY 266 AGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 389
QY 386 TGTCAAGTGTCTCTCAAAATTTGGCAGAAAGTGGTGAAGTCCGTATGCCCGCTGAATC 445
Db 390 TGTCAAGTGTCTCTCAAAATTTGGCAGAAAGTGGTGAAGTCCGTATGCCCGCTGAATC 449
QY 446 TCTGGCTGACTTTTGTGGTGGCCCTTATGTGTGCTGGGCAATTAATAATGGCTCTTT 505
Db 450 TCTGGCTGACTTTTGTGGTGGCCCTTATGTGTGCTGGGCAATTAATAATGGCTCTTT 509
QY 506 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565
Db 510 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 569
QY 566 CATATTTAAGTTCCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAAGCACTCGAG 625
Db 570 CATATTTAAGTTCCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAAGCACTCGAG 629
QY 626 GACAGAAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 685
Db 630 GACAGAAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 689
QY 686 AATTCAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 745
Db 690 AATTCAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 749
QY 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGATTTGCAAAAGAAAGACGAGGAGAGTGGTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGATTTGCAAAAGAAAGACGAGGAGAGTGGTGTCAAAATCTTTGACG 869
QY 866 GCACAGATGCCCTGTGACTCCGGTTCTGACTTTTGAAGGAGGTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCCTGTGACTCCGGTTCTGACTTTTGAAGGAGGTGTTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCTGCAC 985
Db 930 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGATCCCTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGATCCCTTTCATAGGAGAAC 1049
QY 1046 ACACGTAGGAGATACCTGAAGAAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAAC 1105
Db 1050 ACACGTAGGAGATACCTGAAGAAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAAC 1109
QY 1106 CAGATAAAATCAATTGAAGTAAAGGTAAAGCTAGTCTC 1146

Db 1110 CAGATAAAATCAATTGAAGTAAATAAGGTAAAGCTAGTCTC 1150
RESULT 6
US-09-159-812-107
; Sequence 107, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428CS
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-107
Query Match 93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGGCCTGGCCCCGGGCCCGTTCTGTGCTATGGTCTTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCCGGGCCCGTTCTGTGCTATGGTCTTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGCGG 145
Db 90 CGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGCGG 149
QY 146 GCAAGCGTCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGCGGCGTC 205
Db 150 GCAAGCGTCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGCGGCGTC 209
QY 206 TGTCAAGCGGTCCGATGTGCTGGAGCCCTTCCCGCGCGGTGTCTGCGGAACTCC 265
Db 210 TGTCAAGCGGTCCGATGTGCTGGAGCCCTTCCCGCGCGGTGTCTGCGGAACTCC 269
QY 266 AGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 389
QY 386 TGTCAAGTGTCTCTCAAAATTTGGCAGAAAGTGGTGAAGTCCGTATGCCCGCTGAATC 445
Db 390 TGTCAAGTGTCTCTCAAAATTTGGCAGAAAGTGGTGAAGTCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTTGTGGTGGCCCTTATGTGTGCACTGGGCATTAATAATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTTGTGGTGGCCCTTATGTGTGCACTGGGCATTAATAATGGCTCTTT 509
QY 506 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565
Db 510 TTGACCGCACACGCACCTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 569
QY 566 CATATTTAAGTTCCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAAGCACTCGAG 625
Db 570 CATATTTAAGTTCCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAAGCACTCGAG 629
QY 626 GACAGAAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 685
Db 630 GACAGAAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 689
QY 686 AATTCAAGTCTGATGAACCTTCCCAATCAGATGAGCATGATGATGGCCAGAAAGTGAAGA 745

Db 690 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG 749
QY 746 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGATTTGCAAAGAAGACGGAAGCAGAGTGTTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGATTTGCAAAGAAGACGGAAGCAGAGTGTTGTCAAAATCTTTGACG 869
QY 866 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGAGCCCCCCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGAGCCCCCCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAAGGGATCCTTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAAGGGATCCTTTTCATAGGAGAAC 1049
QY 1046 ACACGTAGGAGATACITGAAAGAAATTTGGATTACGCCGCGAAGAGATTTTATCAGCTTAACT 1105
Db 1050 ACACGTAGGAGATACITGAAAGAAATTTGGATTACGCCGCGAAGAGATTTTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 7

US-09-636-215-107
; Sequence 107, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-107

Query Match 93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGGCCTGGCCCGGCCCCGTTCTGTGCTATGGTCTCGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCGGCCCCGTTCTGTGCTATGGTCTCGGCTGACTTCGGGG 89

QY 86 CGCGTGTGTACGCGTGGACCGCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG 145
Db 90 CGCGTGTGTACGCGTGGACCGCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG 149
QY 146 GCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGCGGCGTC 209
QY 206 TGTGCAAGCGGTCGGATGTGTCTGCTGGAGCCCTTCCGCCGCGGTGTCTATGAGGAACTCC 265
Db 210 TGTGCAAGCGGTCGGATGTGTCTGCTGGAGCCCTTCCGCCGCGGTGTCTATGAGGAACTCC 269
QY 266 AGCTGGGCCACAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCACAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 389
QY 386 TGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 445
Db 390 TGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTGTGTGGTGGCTTATGTGTGCACTGGGCATTTAATGGCTCTTT 505
Db 450 TCCTGGCTGACTTGTGTGGTGGCTTATGTGTGCACTGGGCATTTAATGGCTCTTT 509
QY 506 TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATGATGCAAAATATGGTGGAAGAACAG 565
Db 510 TTGACCGCACACGCACTGCAAGGGTCAGGTCAATGATGCAAAATATGGTGGAAGAACAG 569
QY 566 CATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 625
Db 570 CATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 685
Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 689
QY 686 AATTCAATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAAAGACTTG 745
Db 690 AATTCAATGGCTGTGGAGCAATAGAACCCAGTCTACGAGCTGCTGATCAAAAGACTTG 749
QY 746 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGATTTGCAAAGAAGACGGAAGCAGAGTGTTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGATTTGCAAAGAAGACGGAAGCAGAGTGTTGTCAAAATCTTTGACG 869
QY 866 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGAGCCCCCCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGCAGACGTCGAGCCCCCCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAAGGGATCCTTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAAGGGATCCTTTTCATAGGAGAAC 1049
QY 1046 ACACGTAGGAGATACITGAAAGAAATTTGGATTACGCCGCGAAGAGATTTTATCAGCTTAACT 1105
Db 1050 ACACGTAGGAGATACITGAAAGAAATTTGGATTACGCCGCGAAGAGATTTTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

```
RESULT 8
US-09-685-166A-107
; Sequence 107, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-107

Query Match      93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGCTCGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGCTCGGCTGACTTCGGGG 89

QY 86 CGCGTGTGGTACGCGTGAGCCGGCCCCGGCTCCCGCTACACGTGAGCCGCTTGGGCCGGG 145
Db 90 CGCGTGTGGTACGCGTGAGCCGGCCCCGGCTCCCGCTACACGTGAGCCGCTTGGGCCGGG 149

QY 146 GCAAGCGCTCGTAGTGTGACCTGAAGCAGCCGCGGGAGCCGCGTGTGCTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGACCTGAAGCAGCCGCGGGAGCCGCGTGTGCTGCGGCGTC 209

QY 206 TGTGCAAGCGGTGCGATGTGCTGAGCCCTTCCGCGCGGTGTATGAGAGAACTCC 265
Db 210 TGTGCAAGCGGTGCGATGTGCTGAGCCCTTCCGCGCGGTGTATGAGAGAACTCC 269

QY 266 AGCTGGGCCAGAGATTCTGACGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGACGGGAAATCCAAAGCTTATTTATGCCAGGCTGAGTG 329

QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGTTAGTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGTTAGTGGCCACGATATCAACTATTGGCTT 389

QY 386 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAATTTGGCAGAGTGGTGAATCCGTATGCCCGCTGAATC 449

QY 446 TCCTGGCTGACTTGTGCTGGTGGCCTTATGTGCTGCTGGCATTATATGCTGCTTT 505
Db 450 TCCTGGCTGACTTGTGCTGGTGGCCTTATGTGCTGCTGGCATTATATGCTGCTTT 509

QY 506 TTGACCGCACACGCACTGGCAAGGGTCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565
```

```
Db 510 TTGACCGCACACGCACTGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 569
QY 566 CATATTTAAGTCTTTTCTGTGTGAAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 625
Db 570 CATATTTAAGTCTTTTCTGTGTGAAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATAGACTTACAGGACAGCAGATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATAGACTTACAGGACAGCAGATGGGG 689
QY 686 AATTTCATGGCTGTTGGAGCAATAGAACCCCGTCTTACGAGCTGCTGATCAAAGGACTTG 745
Db 690 AATTTCATGGCTGTTGGAGCAATAGAACCCCGTCTTACGAGCTGCTGATCAAAGGACTTG 749
QY 746 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGTAATTGCAAGAAGACGAAAGGAGAGTGGTGTCAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTAATTGCAAGAAGACGAAAGGAGAGTGGTGTCAAATCTTTGACG 869
QY 866 GCACAGATGCTGTGACTCCGGTCTGACTTTTGGAGGAGTGTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCTGTGACTCCGGTCTGACTTTTGGAGGAGTGTGTTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCACTGAGGAGCAGGACGTGAGCCCGCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCACTGAGGAGCAGGACGTGAGCCCGCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTCAAAGGGATCCTTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTCAAAGGGATCCTTTTCATAGGAGAAC 1049
QY 1046 ACACGTGAGGAGATACCTGAAGAAATTTGGATTACGCGCGAAGAGATTTATCAGCTTAACT 1105
Db 1050 ACACGTGAGGAGATACCTGAAGAAATTTGGATTACGCGCGAAGAGATTTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTGAAAGTAATAAGGTAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTGAAAGTAATAAGGTAAGCTAGTCTC 1150

RESULT 9
US-09-115-453-107
; Sequence 107, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-107
```

```
Query Match      93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGCTGCTGCTGCTGCTGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGCTGCTGCTGCTGCTGGGG 89

QY 86 CGCGTGTGGTACGCGTGAGCCGGCCCCGGCTCCCGCTACACGTGAGCCGCTTGGGCCGGG 145
```


||||| 90 CGCGTGTGTACGCTGGACCGGCCCGCTCCCGCTACGAGTGAGCCGCTTGGGCCGGG 149
QY 146 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCGCGGGAGCCGCGTGTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCGCGGGAGCCGCGTGTGCGGCGTC 209
QY 206 TGTGCAAGCGGTGCGATGTGCTGGAGCCCTTCGCGCGGTGTATGGAGAAACTCC 265
Db 210 TGTGCAAGCGGTGCGATGTGCTGGAGCCCTTCGCGCGGTGTATGGAGAAACTCC 269
QY 266 AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGGCTTATTTATGCCAGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGGCTTATTTATGCCAGCTGAGTG 329
QY 326 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGCCACGATATCAACTATTGGCTT 385
Db 330 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGCCACGATATCAACTATTGGCTT 389
QY 386 TGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGTGAGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGTGAGAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGACCTGGGCAATTATATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGACCTGGGCAATTATATGGCTCTTT 509
QY 506 TTGACCGCACACGCACTGCGAAGGTCAGGTCAATGATGCAATATGTTGGAAGGAACAG 565
Db 510 TTGACCGCACACGCACTGCAAGGTCAGGTCAATGATGCAATATGTTGGAAGGAACAG 569
QY 566 CATATTTAAGTTCTTTCTGTTGAAAACCTCAGAAATCGAGTCTGTGGAAGCACCTCGAG 625
Db 570 CATATTTAAGTTCTTTCTGTTGAAAACCTCAGAAATCGAGTCTGTGGAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 689
QY 686 AATTGATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745
Db 690 AATTGATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749
QY 746 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 809
QY 806 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAGGACAGAGTGGTGTCAAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAGGACAGAGTGGTGTCAAAATCTTTGACG 869
QY 866 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 925
Db 870 GCACAGATGCCTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACA 929
QY 926 ACAAGGAACGGGCTCGTTTATCACCATGAGGAGGAGGACGTGAGCCCCCGCCTGCAC 985
Db 930 ACAAGGAACGGGCTCGTTTATCACCATGAGGAGGAGGACGTGAGCCCCCGCCTGCAC 989
QY 986 CTCTGCTGTTAAACACCCAGCCCATCCCTTCTTTCAAAAGGGATCCCTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCAGCCCATCCCTTCTTTCAAAAGGGATCCCTTTCATAGGAGAAC 1049
QY 1046 AACTGAGGAGATCTTGAAGAAATTTGGATTACGCCGGAAGAGATTATCAGCTTAACT 1105
Db 1050 AACTGAGGAGATCTTGAAGAAATTTGGATTACGCCGGAAGAGATTATCAGCTTAACT 1109
QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 10

US-09-688-489-107
; Sequence 107, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-107

Query Match 93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGCTGGCCCCCGGCTTCTGTGCTATGGTCTCGGCTGACTTCCGGG 85
Db 30 TGGAGCTGTCCGCTGGCCCCCGGCTTCTGTGCTATGGTCTCGGCTGACTTCCGGG 89
QY 86 CGCGTGTGTACCGCTGGACCGGCCCGCTCCGCTACGACGTGAGCCGCTTGGGCCGGG 145
Db 90 CGCGTGTGTACCGCTGGACCGGCCCGCTCCGCTACGACGTGAGCCGCTTGGGCCGGG 149
QY 146 GCAAGCGCTCGTAGTGTGCTGAGCCTGAAGCAGCCGCGGGAGCCGCGTGTGCGGCGTC 205
Db 150 GCAAGCGCTCGTAGTGTGAGCCTGAAGCAGCCGCGGGAGCCGCGTGTGCGGCGTC 209
QY 206 TGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTCCGCGCGGTGTATGGAGAAACTCC 265
Db 210 TGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTCCGCGCGGTGTATGGAGAAACTCC 269
QY 266 AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGGCTTATTTATGCCAGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGGCTTATTTATGCCAGCTGAGTG 329
QY 326 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTGGCTT 389
QY 386 TGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGTGAGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGTGAGAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGCTGACTGGGCAATTATATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGCTGACTGGGCAATTATATGGCTCTTT 509
QY 506 TTGACCGCACACGCACTGCGAAGGTCAGGTCAATGATGCAATATGTTGGAAGGAACAG 565
Db 510 TTGACCGCACACGCACTGACAAGGTCAGGTCAATGATGCAATATGTTGGAAGGAACAG 569
QY 566 CATATTTAAGTTCTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGAAGCACCTCGAG 625
Db 570 CATATTTAAGTTCTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGAAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCATGGGG 689
QY 686 AATTGATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745
Db 690 AATTGATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749
QY 746 GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 805

D _b	750	 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGATTGCCAGAAATGAAGA	809
Q _y	806	 AGAA GTTTGCAGATGTATTTCCAAAGAAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACG	865
D _b	810	 AGAA GTTTGCAGATGTATTTCCAAAGAAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACG	869
Q _y	866	 GCACAGATGCCTGTGTGACTCCGGTTCTGAC TTTT GAGGAGGTTGTTTCATCATGATCACA	925
D _b	870	 GCACAGATGCCTGTGTGACTCCGGTTCTGAC TTTT GAGGAGGTTGTTTCATCATGATCACA	929
Q _y	926	 ACAAGGAACGGGGCTCGTTTATCAC CAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCAC	985
D _b	930	 ACAAGGAACGGGGCTCGTTTATCAC CAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCAC	989
Q _y	986	 CTCTGCTGTTAAACACCCAGCCCATCCC TTCTTTCAAAGGGATCCTTTTCATAGGAGAAC	1045
D _b	990	 CTCTGCTGTTAAACACCCAGCCCATCCC TTCTTTCAAAGGGATCCTTTTCATAGGAGAAC	1049
Q _y	1046	 ACACTGAGGAGATACTTTGAAGAATTTGGATT CAGCCGCGAAGAGATTTATCAGCTTAAC T	1105
D _b	1050	 ACACTGAGGAGATACTTTGAAGAATTTGGATT CAGCCGCGAAGAGATTTATCAGCTTAAC T	1109
Q _y	1106	 CAGATAAAAATCATTGAAAGTAATAAGGTA AAAAGCTAGTCTC	1146
D _b	1110	 CAGATAAAAATCATTGAAAGTAATAAGGTA AAAAGCTAGTCTC	1150

RESULT 11

RESOLUT II
US-09-679-426-107.

US-93-873-428-107
; Sequence 107, Application US/09679426

; sequence 101, Appl
; Patent No. 6759515; PATENT NO. 6759515
: GENERAL INFORMATION:

APPLICANT: Xu. Jianachun

APPLICANT: XU, JIANGCHUN
APPLICANT: PILLON, DAVIN C.

APPLICANT: MITCHAM, JENNIFER L.
APPLICANT: MITCHAM, JENNIFER L.
APPLICANT: MITCHAM, JENNIFER L.

APPLICANT: MICHAEL, JENNIFER L.
APPLICANT: Harlocker, Susan L.

APPLICANT: Hailocker, Susan
APPLICANT: Jiana, Yumui

APPLICANT: Jiang, Yuqi
Henderson. Robert A.

APPLICANT: HEINDELSON, ROBERT D.
APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary
APPLICANT: Retter, Marc

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

REFUGANT: VEDAVICK, THOMAS
; APPLICANT: CARTER, DARRICK

; APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: **Skeiky, Yasir A.W.**

APPLICANT: Hepler, William

1. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C20

; CURRENT APPLICATION NUMBER: US/09/679,426

; CURRENT FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

```

;
; TYPE: DNA
;

```

ORGANISM: Homo sapien

US-09-679-426-107

Query Match	93.4%	Score 1070;	DB 4;	Length 1621;
Best Local Similarity	99.9%	Pred. NO. 0;		
Matches 1120; Conservative	0;	Mismatches	1;	Indels 0;
		Gaps	0;	

RESULT 12
US-09-759-143-107

```
; Sequence 107, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107

Query Match      93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGGTCCTGGCTGACTTCGGGG 85
Db  |||||||
QY 30 TGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGTGCTATGGTCCTGGCTGACTTCGGGG 89
Db  |||||||

QY 86 CGCGTGTGGTACGCGTGACCGGCCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGGG 145
Db  |||||||
QY 90 CGCGTGTGGTACGCGTGACCGGCCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCGGG 149
Db  |||||||

QY 146 GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCGGGGAGCCGCGCTGCTGCGGCGTC 205
Db  |||||||
QY 150 GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCGGGGAGCCGCGCTGCTGCGGCGTC 209
Db  |||||||

QY 206 TGTCAAGCGGTCCGGATGTGCTGTGGAGCCCTCCGCGCGGGTGTCTATGGAGAACTCC 265
Db  |||||||
QY 210 TGTCAAGCGGTCCGGATGTGCTGTGGAGCCCTCCGCGCGGGTGTCTATGGAGAACTCC 269
Db  |||||||

QY 266 AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325
Db  |||||||
QY 270 AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329
Db  |||||||

QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTGGCTT 385
Db  |||||||
QY 330 GATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTGGCTT 389
Db  |||||||

QY 386 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATGCCCGCTGAATC 445
Db  |||||||
QY 390 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATGCCCGCTGAATC 449
Db  |||||||

QY 446 TCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGCACTGGGCATTATATGCTCTTT 505
Db  |||||||
QY 450 TCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGCACTGGGCATTATATGCTCTTT 509
Db  |||||||

QY 506 TTGACCGCACACGCACTGGCAAGGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG 565
Db  |||||||
QY 510 TTGACCGCACACGCACTGGCAAGGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG 569
Db  |||||||
```

```
QY 566 CATATTTAAGTTCTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db  |||||||
QY 570 CATATTTAAGTTCTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629
Db  |||||||

QY 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGAGATGGG 685
Db  |||||||
QY 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGAGATGGG 689
Db  |||||||

QY 686 AATTCAATGGCTGTTGGAGCAATAGAACCCCACTTCTACGAGTCTGTATCAAAAGACTTG 745
Db  |||||||
QY 690 AATTCAATGGCTGTTGGAGCAATAGAACCCCACTTCTACGAGTCTGTATCAAAAGACTTG 749
Db  |||||||

QY 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCCAAGAAATGAAGA 805
Db  |||||||
QY 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCCAAGAAATGAAGA 809
Db  |||||||

QY 806 AGAAGTTTGCAGATGTATTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAATCTTTTGACG 865
Db  |||||||
QY 810 AGAAGTTTGCAGATGTATTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAATCTTTTGACG 869
Db  |||||||

QY 866 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGAAGAGGTTGTTTCATCATGATCACA 925
Db  |||||||
QY 870 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGAAGAGGTTGTTTCATCATGATCACA 929
Db  |||||||

QY 926 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGACGAGCGTGGAGCCCCCGCTGCAC 985
Db  |||||||
QY 930 ACAAGGAACGGGCTCGTTTATCACCAGTGAAGGACGAGCGTGGAGCCCCCGCTGCAC 989
Db  |||||||

QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC 1045
Db  |||||||
QY 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC 1049
Db  |||||||

QY 1046 ACACAGGAGATGATCTTGAAGAAATTTGGATTGAGCCCGGAGAGATTTATCAGCTTAAC 1105
Db  |||||||
QY 1050 ACACAGGAGATGATCTTGAAGAAATTTGGATTGAGCCCGGAGAGATTTATCAGCTTAAC 1109
Db  |||||||

QY 1106 CAGATAAAATCATTTGAAAGTAATAAGTAAAGTAAAGCTAGTCTC 1146
Db  |||||||
QY 1110 CAGATAAAATCATTTGAAAGTAATAAGTAAAGTAAAGCTAGTCTC 1150
Db  |||||||

RESULT 13
US-09-651-236-107
; Sequence 107, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
```

; ORGANISM: Homo sapien									
US-09-651-236-107									
Query Match 93.4%; Score 1070; DB 4; Length 1621;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	26	TGAGACTGTCCGGCCTGGCCCGGGCCCGTTC	TGTCGTATGGTCTGGCTGAC	TTCCGGG	85				
Db	30	TGGAGCTGTCCGGCCTGGCCCGGGCCCGTTC	TGTCGTATGGTCTGGCTGAC	TTCCGGG	89				
QY	86	CGGTGTGTACGCGTGGACCGCCCGGCTCCCG	CTACGACGTGAGCCGCTTGGSCCGG	145					
Db	90	CGGTGTGTACGCGTGGACCGCCCGGCTCCCG	CTACGACGTGAGCCGCTTGGSCCGG	149					
QY	146	GCAAGCGCTCGTAGTCTGACCTGAAGCAGCC	CGCGGGAGCCCGTGTGCGCGCTC	205					
Db	150	GCAAGCGCTCGTAGTCTGACCTGAAGCAGCC	CGCGGGAGCCCGTGTGCGCGCTC	209					
QY	206	TGTCAAGCGGTGGATGTGCTGGTGGAGCCCT	TCCGCCCGGTGTATGGAGAACTCC	265					
Db	210	TGTCAAGCGGTGGATGTGCTGGTGGAGCCCT	TCCGCCCGGTGTATGGAGAACTCC	269					
QY	266	AGCTGGGCCCAGAGATTCTGCAGCGGGAATA	CCAAAGCTTATTTATGCCAGGCTGAGTG	325					
Db	270	AGCTGGGCCCAGAGATTCTGCAGCGGGAATA	CCAAAGCTTATTTATGCCAGGCTGAGTG	329					
QY	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTT	AGCTGGCCACGATATCAACTATTTGGCTT	385					
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTT	AGCTGGCCACGATATCAACTATTTGGCTT	389					
QY	386	TGTCAGGTGTTCTCTCAAAAATTTGGCAGAA	TGGTGAGAAATCCGATGCCCGCTGAATC	445					
Db	390	TGTCAGGTGTTCTCTCAAAAATTTGGCAGAA	TGGTGAGAAATCCGATGCCCGCTGAATC	449					
QY	446	TCCTGGCTGACTTTGCTGGTGGCCCTTATGT	GTGCACTGGGCATTATAATGGCTCTTT	505					
Db	450	TCCTGGCTGACTTTGCTGGTGGCCCTTATGT	GTGCACTGGGCATTATAATGGCTCTTT	509					
QY	506	TTGACCGCACACGCACCTGGCAAGGTCAGGT	CATTGATGCAAAATATGGTGAAGGAACAG	565					
Db	510	TTGACCGCACACGCACCTGGCAAGGTCAGGT	CATTGATGCAAAATATGGTGAAGGAACAG	569					
QY	566	CATATTTAAGTTCCTTTCTGTGGAATACTC	AGAAATCGAGTCTGTGGGAAGCACCTCGAG	625					
Db	570	CATATTTAAGTTCCTTTCTGTGGAATACTC	AGAAATCGAGTCTGTGGGAAGCACCTCGAG	629					
QY	626	GACAGAACATGTTGGATGGTGAGCACCTTT	CTATACGACTTACAGGACAGCAGATGGGG	685					
Db	630	GACAGAACATGTTGGATGGTGAGCACCTTT	CTATACGACTTACAGGACAGCAGATGGGG	689					
QY	686	AATTCATGGCTGTTGGAGCAATAGAAACCC	AGTTCTACGAGCTGCTGATCAAAGGACTTG	745					
Db	690	AATTCATGGCTGTTGGAGCAATAGAAACCC	AGTTCTACGAGCTGCTGATCAAAGGACTTG	749					
QY	746	GACTAAAGTCTGATGAACCTTCCCAATCAG	ATGAGCATGGATGGCCAGAAATGAAGA	805					
Db	750	GACTAAAGTCTGATGAACCTTCCCAATCAG	ATGAGCATGGATGGCCAGAAATGAAGA	809					
QY	806	AGAACTTTGCAGATGTATTTGCAAAAGAAG	ACGAAGGCAGAGTGGTCAAAATCTTTGACG	865					
Db	810	AGAACTTTGCAGATGTATTTGCAAAAGAAG	ACGAAGGCAGAGTGGTCAAAATCTTTGACG	869					
QY	866	GCACAGATGCCTGTGTGACTCCGGTCTGAC	TTTTTGGAGAGGTTGTTTCATCATGATCACA	925					
Db	870	GCACAGATGCCTGTGTGACTCCGGTCTGAC	TTTTTGGAGAGGTTGTTTCATCATGATCACA	929					
QY	926	ACAAAGAACGGGCTCGTTTTATCACCAGT	GAGGACGACGTCGAGCCCCCGCTGAC	985					
Db	930	ACAAAGAACGGGCTCGTTTTATCACCAGT	GAGGACGACGTCGAGCCCCCGCTGAC	989					
QY	986	CTCTGCTGTTAAACACCCCGCATCCCTTCT	TTTCAAAAGGGATCCTTTTCATAGGAGAAC	1045					

Db	990	CTCTGCTGTTAAACACCCAGCCATCCCTTCT	TTTCAAAAGGGATCCTTTTCATAGAGAAC	1049					
QY	1046	ACACTGAGGAGATACTTGAAGAAATTTGGAT	TCAGCCGGAAGAGATTTTATCAGCTTAACT	1105					
Db	1050	ACACTGAGGAGATACTTGAAGAAATTTGGAT	TCAGCCGGAAGAGATTTTATCAGCTTAACT	1109					
QY	1106	CAGATAAAATCATTTGAAAAGTAATAAGGT	AAAAAGCTAGTCTC	1146					
Db	1110	CAGATAAAATCATTTGAAAAGTAATAAGGT	AAAAAGCTAGTCTC	1150					
RESULT 14									
US-09-020-956-2									
; Sequence 2, Application US/09020956									
; Patent No. 6261562									
; GENERAL INFORMATION:									
; APPLICANT: Xu, Jiangchun									
; APPLICANT: Dillin, Davin C.									
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO									
; NUMBER OF SEQUENCES: 178									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: SEED and BERRY LLP									
; STREET: 6300 Columbia Center, 701 Fifth Avenue									
; CITY: Seattle									
; STATE: WA									
; COUNTRY: USA									
; ZIP: 98104									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: PatentIn Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/09/020,956									
; FILING DATE: 09-FEB-1998									
; CLASSIFICATION:									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Maki, David J.									
; REGISTRATION NUMBER: 31,392									
; REFERENCE/DOCKET NUMBER: 210121.427C2									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: (206) 622-4900									
; TELEFAX: (206) 682-6031									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 816 base pairs									
; TYPE: nucleic acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: cdna									
US-09-020-956-2									
Query Match 34.7%; Score 398; DB 3; Length 816;									
Best Local Similarity 100.0%; Pred. No. 7.3e-195;									
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	634	ATGTTGGATGGTGGAGCACCTTTCTATACGAC	TTACAGGACAGCAGATGGGGAATTCATG	693					
Db	7	ATGTTGGATGGTGGAGCACCTTTCTATACGAC	TTACAGGACAGCAGATGGGGAATTCATG	66					
QY	694	GCTGTTGGAGCAATAGAAACCCAGTTCTAC	GAGCTGCTGATCAAAGGACTTGGACTAAAG	753					
Db	67	GCTGTTGGAGCAATAGAAACCCAGTTCTAC	GAGCTGCTGATCAAAGGACTTGGACTAAAG	126					
QY	754	TCTGATGAACCTTCCCAATCAGATGAGCAT	GGATGGATGGCCAGAAATGAAGAAGATT	813					
Db	127	TCTGATGAACCTTCCCAATCAGATGAGCAT	GGATGGATGGCCAGAAATGAAGAAGATT	186					
QY	814	GCAGATGTATTTGCAAGAAGACGAAGGC	AGAGTGGTGTCAAATCTTTGACGGCACAGAT	873					
Db	187	GCAGATGTATTTGCAAGAAGACGAAGGC	AGAGTGGTGTCAAATCTTTGACGGCACAGAT	246					
QY	874	GCCTGTGTGACTCCCGGTTCTGACTTTTG	AGGAGGTTGTTTCATCATGATCAACAAGGAA	933					

Db 247 GCCTGTGTGACTCCGGTCTGACTTTTGGAGGAGGTGTTTCATCATGATCACAACAAGGAA 306
QY 934 CGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTG 993
Db 307 CGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTG 366
QY 994 TTAAACACCCCGCCATCCCTTCTTTCAAAGGGATCC 1031
Db 367 TTAAACACCCCGCCATCCCTTCTTTCAAAGGGATCC 404

RESULT 15
US-09-030-607-2
; Sequence 2, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-030-607-2

Query Match 34.7%; Score 398; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 7.3e-195;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 634 ATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGACAGCAGATGGGGAATTCATG 693
Db 7 ATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGACAGCAGATGGGGAATTCATG 66
QY 694 GCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAG 753
Db 67 GCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAG 126
QY 754 TCTGATGAACCTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGAAGATT 813
Db 127 TCTGATGAACCTCCCAATCAGATGAGCATGGATGATGGCCAGAAATGAAGAAGATT 186
QY 814 GCAGATGTATTTGCAAAGAACGAGGACAGTGGTGTCAAATCTTTGACGGCACAGAT 873
Db 187 GCAGATGTATTTGCAAAGAACGAGGACAGTGGTGTCAAATCTTTGACGGCACAGAT 246

QY 874 GCCTGTGTGACTCCGGTCTGACTTTTGGAGGAGGTGTTTCATCATGATCACAACAAGGAA 933
Db 247 GCCTGTGTGACTCCGGTCTGACTTTTGGAGGAGGTGTTTCATCATGATCACAACAAGGAA 306
QY 934 CGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTG 993
Db 307 CGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTG 366
QY 994 TTAAACACCCCGCCATCCCTTCTTTCAAAGGGATCC 1031
Db 367 TTAAACACCCCGCCATCCCTTCTTTCAAAGGGATCC 404

Search completed: July 27, 2005, 10:59:48
Job time : 234 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 27, 2005, 02:28:10 ; Search time 701 Seconds
(without alignments)
9677.637 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: . 1 atggcactgcaggcatctc.....ataaggtaaaagctagtctc 1146

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1146	100.0	2005	6	AAD38607	Aad38607 Human alp
2	1146	100.0	2005	6	AAD38603	Aad38603 Human alp
3	1146	100.0	2005	10	ADD18532	Add18532 Human pro
4	1146	100.0	2040	13	ACN38207	Acn38207 Tumour-as
5	1146	100.0	2069	6	AAD38604	Aad38604 Human alp
6	1146	100.0	2069	10	ADB75193	Adb75193 Prostate
7	1132	98.8	3654	6	AAD38605	Aad38605 Human alp
8	1132	98.8	3654	10	ADB75195	Adb75195 Prostate
9	1095	95.5	2069	10	ADB75201	Adb75201 Prostate
10	1081	94.3	2626	10	ADB75203	Adb75203 Prostate
11	1070	93.4	1621	2	AAV58584	Aav58584 Prostate
12	1070	93.4	1621	2	AAV61199	Aav61199 Full leng
13	1070	93.4	1621	3	AAA06347	Aaa06347 Human imm
14	1070	93.4	1621	3	ABS71252	Abs71252 Human pro
15	1070	93.4	1621	4	AAH93463	Aah93463 Human pro
16	1070	93.4	1621	4	AAS63555	Aas63555 Human pro
17	1070	93.4	1621	4	AAH02528	Aah02528 Prostate
18	1070	93.4	1621	4	AAH84777	Aah84777 Human pro
19	1070	93.4	1621	5	ACA59364	Aca59364 Prostate
20	1070	93.4	1621	5	AAS10106	Aas10106 Human pro

21	1070	93.4	1621	6	ABL94927	Ab194927 Human Fl-
22	1070	93.4	1621	6	ABS58636	Abs58636 Prostate
23	1070	93.4	1621	8	ACC95091	Acc95091 Prostate
24	1070	93.4	1621	10	ADB13557	Adb13557 Human pro
25	1070	93.4	1621	10	ADG26973	Adg26973 Human pro
26	1070	93.4	2376	5	ABV25239	Abv25239 Human pro
27	1070	93.4	2376	5	ABV21293	Abv21293 Human pro
28	1070	93.4	2376	5	ABV21881	Abv21881 Human pro
29	1070	93.4	2376	5	ABV27112	Abv27112 Human pro
30	1019	88.9	1674	4	AAH13696	Aah13696 Human CDN
31	797	69.5	1294	5	ABV22733	Abv22733 Human pro
32	797	69.5	1294	5	ABV28442	Abv28442 Human pro
33	797	69.5	1294	5	ABV28544	Abv28544 Human pro
34	797	69.5	1294	5	ABV22620	Abv22620 Human pro
35	797	69.5	1294	5	ABV27711	Abv27711 Human pro
36	756	66.0	1039	4	AAC91303	Aac91303 Human pol
37	740	64.6	1316	10	ADB75199	Adb75199 Prostate
38	613	53.5	1317	4	AAH17637	Aah17637 Human CDN
39	595	51.9	2946	10	ADB75205	Adb75205 Prostate
40	595	51.9	2946	12	ADP56742	Adp56742 Human alp
41	595	51.9	3023	6	AAD38606	Aad38606 Human alp
42	595	51.9	3023	10	ADB75197	Adb75197 Prostate
43	524	45.7	720	4	AAH03341	Aah03341 Human CDN
44	498	43.5	729	12	ADP56741	Adp56741 Human alp
45	493	43.0	865	5	ABV28560	Abv28560 Human pro

ALIGNMENTS

RESULT 1
AAD38607
ID AAD38607 standard; cDNA; 2005 BP.
XX
AC AAD38607;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human alpha-methylacyl-CoA racemase splice variant, SV4 cDNA.
XX
KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW cytostatic; SV4; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 66..1214
FT /*tag= a
FT /product= "Human SV4 protein"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US030532.
XX
PR 28-SEP-2000; 2000US-0236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23975.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase.
XX
PS Claim 54; Fig 9; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether an

CC individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of alpha-
CC methylacyl-CoA racemase. Sequences of the invention are useful in
CC diagnostic methods, drug screening assays, and in treating or preventing
CC cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-
CC acyl-CoA racemase splice variant, SV4 cDNA
XX
SQ Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 U; 0 Other;

Query Match 100.0%; Score 1146; DB 6; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCGTTCTGT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
66 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCGTTCTGT 125

QY 61 GCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGTGACGCTGGACCGCCCGCTCCCGC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
126 GCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGTGACGCTGGACCGCCCGCTCCCGC 185

QY 121 TACGACGTGAGCCGCTTGGSCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
186 TACGACGTGAGCCGCTTGGSCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 245

QY 181 CGGGGAGCCGCGTCTGCGCGCTCTGTGCAAGCGGTGCGATGTCTGCTGAGCCCTTC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
246 CGGGGAGCCGCGTCTGCGCGCTCTGTGCAAGCGGTGCGATGTCTGCTGAGCCCTTC 305

QY 241 CGCCGCGGTGTATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAATAATCCA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
306 CGCCGCGGTGTATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAATAATCCA 365

QY 301 AGGCTATTATGCCAGGCTGAGTGGATTGTGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
366 AGGCTATTATGCCAGGCTGAGTGGATTGTGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425

QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAGTGGT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
426 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAGTGGT 485

QY 421 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCCCTATGTGT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
486 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCCCTATGTGT 545

QY 481 GCAGTGGGCATTATATGCTCTTTTGGCTTTGTGACCGCACACGCACTGGCAAGGTCAGTCA 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
546 GCAGTGGGCATTATATGCTCTTTTGGCTTTGTGACCGCACACGCACTGGCAAGGTCAGTCA 605

QY 541 GATGCAAAATATGGTGGAGGAACAGCAGATATTTAAGTCTTTTCTGTGGAAAATCAGAAA 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
606 GATGCAAAATATGGTGGAGGAACAGCAGATATTTAAGTCTTTTCTGTGGAAAATCAGAAA 665

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 725

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
726 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTTC 785

QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
786 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 845

QY 781 ATGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGATTTGCAAAAGACGAAG 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
846 ATGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGATTTGCAAAAGACGAAG 905

QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTCTGACTTTT 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
906 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTCTGACTTTT 965

QY 901 GAGGAGGTTGTTTCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
966 GAGGAGGTTGTTTCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1025

QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGACATCCCTTCTTTC 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGACATCCCTTCTTTC 1085

QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1086 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1145

QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAAAATCATTTGAAAGTAATAAGGTAAAAAGCT 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAAAAATCATTTGAAAGTAATAAGGTAAAAAGCT 1205

QY 1141 AGTCTC 1146
Db |||||

1206 AGTCTC 1211

RESULT 2
AAD38603
ID AAD38603 standard; cDNA; 2005 BP.
XX
AC AAD38603;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human alpha-methylacyl-CoA racemase SV1 cDNA #1.
XX
KW Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
KW cytosstatic; SV1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 66..1214
FT /*tag= a
FT /product= "Human SV1 protein #1"
FT /note= "This region is specifically claimed as SEQ ID NO:
FT 3 in claim 54 of the specification"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US030532.
XX
PR 28-SEP-2000; 2000US-0236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23971.
XX
XX Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase.
XX
PS Claim 54; Fig 1; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether an
CC individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of alpha-
CC methylacyl-CoA racemase. Sequences of the invention are useful in
CC diagnostic methods, drug screening assays, and in treating or preventing
CC cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-

CC	acyl-CoA racemase SV1 cDNA					
XX						
SQ	Sequence 2005 BP; 519 A; 427 C; 514 G; 545 T; 0 U; 0 Other;					
	Query Match	100.0%;	Score 1146;	DB 6;	Length 2005;	
	Best local Similarity	100.0%;	Pred. No. 0;			
	Matches 1146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGGCACTGCAGGCGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCCGGCCCGTTCGT	60			
Db	66	ATGGCACTGCAGGCGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCCGGCCCGTTCGT	125			
QY	61	GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTAACGCTGGAACCGGCCCGGCTCCGGC	120			
Db	126	GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTAACGCTGGAACCGGCCCGGCTCCGGC	185			
QY	121	TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGCTAGTAGCTGGAACCTGAAGCAGCCG	180			
Db	186	TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGCTAGTAGCTGGAACCTGAAGCAGCCG	245			
QY	181	CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGCTGGAGCCCTTC	240			
Db	246	CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGCTGGAGCCCTTC	305			
QY	241	CGCCGCGGTGTCAATGAGAATACTCCAGCTGGGCCACAGAAATTCTGCAGCGGAAAATCCA	300			
Db	306	CGCCGCGGTGTCAATGAGAATACTCCAGCTGGGCCACAGAAATTCTGCAGCGGAAAATCCA	365			
QY	301	AGGCTTATTATGCCAGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT	360			
Db	366	AGGCTTATTATGCCAGCTGAGTGGATTTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT	425			
QY	361	GGCCACGATATCAACTATTTTGGCTTTGTCAAGTGTTCTCTCAAAAAATTGGCAGAAGTGGT	420			
Db	426	GGCCACGATATCAACTATTTTGGCTTTGTCAAGTGTTCTCTCAAAAAATTGGCAGAAGTGGT	485			
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT	480			
Db	486	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT	545			
QY	481	GCACTGGGCATTATATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAATT	540			
Db	546	GCACTGGGCATTATATATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAATT	605			
QY	541	GATGCAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	600			
Db	606	GATGCAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	665			
QY	601	TCGAGTCTGTGGAAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	660			
Db	666	TCGAGTCTGTGGAAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	725			
QY	661	ACGACTTACAGGACAGCAGATGGGGAATTATGGCTGTTGGAGCAATAGAACCCCAAGTTC	720			
Db	726	ACGACTTACAGGACAGCAGATGGGGAATTATGGCTGTTGGAGCAATAGAACCCCAAGTTC	785			
QY	721	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	780			
Db	786	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	845			
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGACGAAG	840			
Db	846	ATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGACGAAG	905			
QY	841	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	900			
Db	906	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	965			
QY	901	GAGGAGTTGTTTCATCATGATCACAAACAAGGAACCGGGGCTCGTTTTATCACCAAGTACCAG	960			
Db	966	GAGGAGTTGTTTCATCATGATCACAAACAAGGAACCGGGGCTCGTTTTATCACCAAGTACCAG	1025			
QY	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTGTTAAACACCCCAGCCATCCCTTCTTTC	1020			

SQ	Sequence 2005 BP; 520 A; 427 C; 514 G; 544 T; 0 U; 0 Other;									
	Query Match	100.0%;	Score 1146;	DB 10;	Length 2005;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 1146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
QY	1	ATGGCACTGCAGGCGATCTCGGTCTGTTGGAGCTGTCCGGCCCTGGCCCCCGGGCCCGTTCTGT	60							
Db	66	ATGGCACTGCAGGCGATCTCGGTCTGTTGGAGCTGTCCGGCCCTGGCCCCCGGGCCCGTTCTGT	125							
QY	61	GCTATGGTCTGGCTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGC	120							
Db	126	GCTATGGTCTGGCTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGC	185							
QY	121	TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG	180							
Db	186	TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG	245							
QY	181	CGGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCCCTTC	240							
Db	246	CGGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGCCCTTC	305							
QY	241	CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATAATCCA	300							
Db	306	CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATAATCCA	365							
QY	301	AGGCTTATTATGCCAGGCTGAGTGGATTGCGCCACTCAGGAAGCTTCTGCCGGTAGCT	360							
Db	366	AGGCTTATTATGCCAGGCTGAGTGGATTGCGCCACTCAGGAAGCTTCTGCCGGTAGCT	425							
QY	361	GGCCACGATATCAACTATTGCGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT	420							
Db	426	GGCCACGATATCAACTATTGCGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT	485							
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGCTGGTGGCCCTTATGTGT	480							
Db	486	GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTGTGCTGGTGGCCCTTATGTGT	545							
QY	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	540							
Db	546	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	605							
QY	541	GATGCAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	600							
Db	606	GATGCAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	665							
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT	660							
Db	666	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT	725							
QY	661	ACGACTTACAGGACAGCAGATGGGAATTATGGCTGTTGGAGCAATAGAACCCAGTTC	720							
Db	726	ACGACTTACAGGACAGCAGATGGGAATTATGGCTGTTGGAGCAATAGAACCCAGTTC	785							
QY	721	TACGAGCTGCTGATCAAAGCACTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780							
Db	786	TACGAGCTGCTGATCAAAGCACTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	845							
QY	781	ATGGATGATTGGCCAGAAATGAAGAAAGATTGTCAGATGATTTTGCAAAGAACGAAAG	840							
Db	846	ATGGATGATTGGCCAGAAATGAAGAAAGATTGTCAGATGATTTTGCAAAGAACGAAAG	905							
QY	841	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	900							
Db	906	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	965							
QY	901	GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	960							
Db	966	GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	1025							
QY	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCCTCTTTC	1020							
Db	1026	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCCTCTTTC	1085							

QY	1021	AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATT	CAGC	108
Db	1086	AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATT	CAGC	1145
QY	1081	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTA	AAAAGCT	1140
Db	1146	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTA	AAAAGCT	1205
QY	1141	AGTCTC	1146	
Db	1206	AGTCTC	1211	
RESULT 4				
ACN38207				
ID	ACN38207 standard; cDNA; 2040 BP.			
XX	AC	ACN38207;		
XX	DT	18-NOV-2004 (first entry)		
XX	DE	Tumour-associated antigenic target (TAT) cDNA DNA324567, SEQ ID NO:1568.		
KW	KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;		
KW	KW	tumour; diagnosis; cell proliferative disorder; breast cancer;		
KW	KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;		
KW	KW	central nervous system cancer; bladder cancer; pancreatic cancer;		
KW	KW	cervical cancer; melanoma; leukaemia; hybridisation probe;		
KW	KW	chromosome identification; chromosome mapping; gene mapping;		
KW	KW	gene therapy; cytostatic; gene; ss.		
XX	OS	Homo sapiens.		
XX	PN	WO2004030615-A2.		
XX	PD	15-APR-2004.		
XX	PF	29-SEP-2003; 2003WO-US028547.		
XX	PR	02-OCT-2002; 2002US-0414971P.		
XX	PA	(GETH) GENENTECH INC.		
XX	PI	Wu TD, Zhang Z, Zhou Y;		
XX	DR	WPI; 2004-347921/32.		
XX	DR	P-PSDB; ABM80605.		
PT	PT	New tumor-associated antigenic target polypeptides and nucleic acids,		
PT	PT	useful in preparing a medicament for treating or detecting a		
PT	PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or		
PT	PT	prostate cancer or tumor.		
XX	PS	Claim 1; SEQ ID NO 1568; 7273pp; English.		
XX	CC	The invention relates to human tumour-associated antigenic target (TAT)		
CC	CC	polypeptides, and their related nucleic acids. The TAT polypeptides are		
CC	CC	overexpressed in cancer tissues compared to normal tissues, and may thus		
CC	CC	serve as effective targets for the diagnosis and treatment of cancer in		
CC	CC	mammals. The invention also relates to nucleic acid and polypeptide		
CC	CC	sequences at least 80% identical to the TAT nucleic acids and		
CC	CC	polypeptides; expression vectors and host cells comprising a TAT nucleic		
CC	CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic		
CC	CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a		
CC	CC	TAT polypeptide; and methods and compositions for the treatment or		
CC	CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,		
CC	CC	antibodies, antagonists, binding molecules and compositions are useful		
CC	CC	for diagnosing or treating a cell proliferative disorder associated with		
CC	CC	increased TAT expression, particularly cancers such as breast cancer,		
CC	CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder		
CC	CC	cancer, pancreatic cancer, cervical cancer, cancers of the central		
CC	CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be		

CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAR nucleic acid of the invention
XX
SQ Sequence 2040 BP; 524 A; 439 C; 529 G; 548 T; 0 U; 0 Other;
Query Match 100.0%; Score 1146; DB 13; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCCTGGCCCCGGCCCGTTCTGT 60
Db |
Qy 61 GCTATGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCTGGACCGGCCCGGCTCCCGC 120
Db |
Qy 121 TACGACGTGAGCCGCTTGGGCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCG 180
Db |
Qy 181 CGGGAGCCGCGTGTCTGCGGCGCTGTGTGCAAGCGGTGCGATGTCTGCTGGAGCCCTTC 240
Db |
Qy 241 CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db |
Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db |
Qy 361 GGCCACGATATCAACTATTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGT 420
Db |
Qy 421 GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGT 480
Db |
Qy 481 GCATGGGCATTATAATGGCTCTTTTGGACCGCACACGACTGGCAAGGTCAGGTCAAT 540
Db |
Qy 541 GATGAAATATGGTGAAGGAACAGCATATTTAAGTCTTTCTGTGGAAACTCAGAAA 600
Db |
Qy 601 TCGAGTCTGTGGAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db |
Qy 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db |
Qy 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
Db |
Qy 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTTGCAAGAAGACGAAG 840
Db |
Qy 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGACTCCGGTCTGACTTTT 900
Db |
Qy 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db |
990 GAGGAGTGTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049

Qy 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTC 1020
Db |
Qy 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTCAGC 1080
Db |
Qy 1081 CGCGAAGAGATTATCATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGGTAAGAGCT 1140
Db |
Qy 1141 AGTCTC 1146
Db |
Qy 1230 AGTCTC 1235
Db |
RESULT 5
AAD38604
ID AAD38604 standard; cDNA; 2069 BP.
XX
AC AAD38604;
XX 23-SEP-2002 (first entry)
XX Human alpha-methylacyl-CoA racemase SV1 cDNA #2.
DE Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
XX cytosolic; SV1; gene; ss.
OS Homo sapiens;
XX
FH Key Location/Qualifiers
CDS 90..1238
FT /*tag= a
FT /product= "Human SV1 protein #2"
XX
PN WO200227324-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-US030532.
XX
PR 28-SEP-2000; 2000US-0236238P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Richardson J, Monahan J;
XX
DR WPI; 2002-405070/43.
DR P-PSDB; AAE23972.
XX
PT Determining risk for prostate cancer in subject or risk for metastatic
PT prostate cancer to liver or lymph nodes of prostate cancer patients,
PT comprises measuring expression or activity of alpha-methylacyl-CoA
PT racemase.
XX
PS Claim 54; Fig 3; 102pp; English.
XX
CC The present invention relates to novel methods for determining whether an
CC individual is at risk for prostate cancer or whether a prostate cancer
CC patient is at risk for metastatic prostate cancer to the liver or lymph
CC nodes. The method involves measuring the expression or activity of alpha-
CC methylacyl-CoA racemase. Sequences of the invention are useful in
CC diagnostic methods, drug screening assays, and in treating or preventing
CC cancer, e.g. prostate cancer. The present sequence is human alpha-methyl-
CC acyl-CoA racemase SV1 cDNA
SQ Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 U; 0 Other;
Query Match 100.0%; Score 1146; DB 6; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1146;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ATGGCACTGCAGGGCATCTCGGTCTGTTGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT	60							
Db	90	ATGGCACTGCAGGGCATCTCGGTCTGTTGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT	149							
Qy	61	GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACCGCTGGACCGGCCCGGCTCCCGC	120							
Db	150	GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACCGCTGGACCGGCCCGGCTCCCGC	209							
Qy	121	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGAGACCTGAAGCAGCCG	180							
Db	210	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGAGACCTGAAGCAGCCG	269							
Qy	181	CGGGAGCCGCGTGTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGCCCTTC	240							
Db	270	CGGGAGCCGCGTGTGCGGGCTCTGTGCAAGCGGTGCGATGTGCTGCTGAGCCCTTC	329							
Qy	241	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATAATCCA	300							
Db	330	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATAATCCA	389							
Qy	301	AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCTGCCGTTAGCT	360							
Db	390	AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAAAGCTTCTGCCGTTAGCT	449							
Qy	361	GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT	420							
Db	450	GGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT	509							
Qy	421	GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGCCTTATGTGT	480							
Db	510	GAGATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT	569							
Qy	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	540							
Db	570	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	629							
Qy	541	GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCAGAAA	600							
Db	630	GATGCAAAATATGGTGAAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAAACTCAGAAA	689							
Qy	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	660							
Db	690	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	749							
Qy	661	ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC	720							
Db	750	ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC	809							
Qy	721	TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780							
Db	810	TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	869							
Qy	781	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAGAAGACGAAG	840							
Db	870	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAGAAGACGAAG	929							
Qy	841	GCAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT	900							
Db	930	GCAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT	989							
Qy	901	GAGGAGTTGTTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTAGGAG	960							
Db	990	GAGGAGTTGTTTCATCATGATCACAAGGAACGGGGCTCGTTTATCACCAGTAGGAG	1049							
Qy	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCACCCAGCCATCCCTTCTTC	1020							
Db	1050	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCACCCAGCCATCCCTTCTTC	1109							
Qy	1021	AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACITGAAGAATTTGGATTACG	1080							
Db	1110	AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACITGAAGAATTTGGATTACG	1169							

Qy	1081	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT	1144
Db	1170	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT	1229
Qy	1141	AGTCTC	1146
Db	1230	AGTCTC	1235
RESULT 6			
ADB75193	ADB75193		
ID	ADB75193 standard; cDNA; 2069 BP.		
XX			
AC	ADB75193;		
DT	04-DEC-2003 (first entry)		
XX	Prostate cancer marker cDNA.		
DE			
XX	Prostate; cancer; cytostatic; gene therapy; marker; ss.		
KW			
XX	Homo sapiens.		
OS			
XX	WO2003009814-A2.		
PN			
XX			
PD	06-FEB-2003.		
XX			
PF	25-JUL-2002; 2002WO-US023913.		
XX			
PR	25-JUL-2001; 2001US-0307982P.		
PR	22-AUG-2001; 2001US-0314356P.		
PR	25-SEP-2001; 2001US-0325020P.		
PR	12-DEC-2001; 2001US-0341746P.		
PR	05-MAR-2002; 2002US-0362158P.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;		
PI	Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;		
XX			
DR	WPI; 2003-248033/24.		
XX			
PT	New nucleic acid molecule, useful for diagnosing or treating prostate cancer.		
PT			
XX			
PS	Claim 1; SEQ ID NO 17; 99pp; English.		
XX			
CC	The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with a prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SO	Sequence 2069 BP; 553 A; 439 C; 529 G; 548 T; 0 U; 0 Other;		
Query Match			
Query Match		100.0%;	
Best Local Similarity		Pred. No. 0;	
Matches 1146;		Conservative	
		0;	
Mismatches		0;	
		Gaps 0;	

Qy	1	ATGGCACTGCAGGGCATCTCGGTCTGTTGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT	60							
Db	90	ATGGCACTGCAGGGCATCTCGGTCTGTTGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT	149							

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGCTGGACCGGCCCGGCTCCCGC 120
Db |||||
150 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGCTGGACCGGCCCGGCTCCCGC 209

QY 121 TACGACGTGAGCCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCGG 180
Db |||||
210 TACGACGTGAGCCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCGG 269

QY 181 CGGGAGCGCGCGTGTGCTGCGGCGTCTGTCAAGCGGTGCGATGTCTGTGAGCCCTTC 240
Db |||||
270 CGGGAGCGCGCGTGTGCTGCGGCGTCTGTCAAGCGGTGCGATGTCTGTGAGCCCTTC 329

QY 241 CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||
330 CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 389

QY 301 AGGCTTATTATGCCAGGCTGATGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360
Db |||||
390 AGGCTTATTATGCCAGGCTGATGGATTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 449

QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db |||||
450 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAATTGGCAGAAAGTGT 509

QY 421 GAGAAATCGTATGCCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480
Db |||||
510 GAGAAATCGTATGCCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 569

QY 481 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGTCAGGTCAATT 540
Db |||||
570 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGTCAGGTCAATT 629

QY 541 GATGAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTGTGGAAACTCAGAAA 600
Db |||||
630 GATGAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTGTGGAAACTCAGAAA 689

QY 601 TCGAGTCTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGAGCACCTTTCTAT 660
Db |||||
690 TCGAGTCTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGAGCACCTTTCTAT 749

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTC 720
Db |||||
750 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGAGCAATAGAACCCAGTTC 809

QY 721 TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGTGATGAATCTCCCAATCAGATGAGC 780
Db |||||
810 TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGTGATGAATCTCCCAATCAGATGAGC 869

QY 781 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACCAAG 840
Db |||||
870 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACCAAG 929

QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db |||||
930 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 989

QY 901 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db |||||
990 GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049

QY 961 CAGGACGTGAGCCCCCGCCCTGACCTCTGTGTTAAACACCCCGCCATCCCTTTCTTC 1020
Db |||||
1050 CAGGACGTGAGCCCCCGCCCTGACCTCTGTGTTAAACACCCCGCCATCCCTTTCTTC 1109

QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC 1080
Db |||||
1110 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC 1169

QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAAGCT 1140
Db |||||
1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAAGCT 1229

QY 1141 AGTCTC 1146
Db |||||
1230 AGTCTC 1235

RESULT 7
AAD38605
ID AAD38605 standard; cDNA; 3654 BP.
XX
AC AAD38605;
XX 23-SEP-2002 (first entry)
XX Human alpha-methylacyl-CoA racemase splice variant, SV2 cDNA.
DE Human; prostate cancer; alpha-methylacyl-CoA racemase; drug screening;
XX cytostatic; SV2; gene; ss.
KW Homo sapiens.
OS
FH Key Location/Qualifiers
CDS 90..1274
FT /*tag= a
FT /product= "Human SV2 protein"
FT /transl_except= (pos:612..614, aa:Asp)

XX WO200227324-A2.
PN 04-APR-2002.
XX 28-SEP-2001; 2001WO-US030532.
XX 28-SEP-2000; 2000US-0236238P.
XX (MILL-) MILLENNIUM PHARM INC.
PI Richardson J, Monahan J;
XX WPI; 2002-405070/43.
DR P-PSDB; AAE23973.
XX

Determining risk for prostate cancer in subject or risk for metastatic prostate cancer to liver or lymph nodes of prostate cancer patients, comprises measuring expression or activity of alpha-methylacyl-CoA racemase.

Claim 54; Fig 5; 102pp; English.

The present invention relates to novel methods for determining whether an individual is at risk for prostate cancer or whether a prostate cancer patient is at risk for metastatic prostate cancer to the liver or lymph nodes. The method involves measuring the expression or activity of alpha-methylacyl-CoA racemase. Sequences of the invention are useful in diagnostic methods, drug screening assays, and in treating or preventing cancer, e.g. prostate cancer. The present sequence is human alpha-methylacyl-CoA racemase splice variant, SV2 cDNA

Sequence 3654 BP; 1050 A; 751 C; 888 G; 965 T; 0 U; 0 Other;

Query Match 98.8%; Score 1132; DB 6; Length 3654;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCCTGGCCCGGCGGCTCTGT 60
Db |||||
90 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCCTGGCCCGGCGGCTCTGT 149

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGGCCCGGCTCCCGC 120
Db |||||
150 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGGCCCGGCTCCCGC 209

QY 121 TACGACGTGAGCCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCGG 180
Db |||||

Dd	210	TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG	269
Qy	181	CGGGGAGCCGCGTGTGGCGGTCTGTGCAAGCGTGGATGTGCTGGAGCCCTTC	240
Dd	270	CGGGAGCCGCGTGTGGCGGTCTGTGCAAGCGTGGATGTGCTGGAGCCCTTC	329
Qy	241	CGCCGCGGTGTCAATGGAGAACTCCAGCTGGGCCACAGATTTCTGACGGGAAAAATCCA	300
Dd	330	CGCCGCGGTGTCAATGGAGAACTCCAGCTGGGCCACAGATTTCTGACGGGAAAAATCCA	389
Qy	301	AGGCTTATTTATGCCAGGTGAGTGGATTTGGCCCACTCAGGAAGCTTCTGCCGTTAGCT	360
Dd	390	AGGCTTATTTATGCCAGGTGAGTGGATTTGGCCCACTCAGGAAGCTTCTGCCGTTAGCT	449
Qy	361	GGCCACGATATCAACTATTGGCTTTGTGCAGGTGTCTCTCAAAAATTGGCAGAAAGTGGT	420
Dd	450	GGCCACGATATCAACTATTGGCTTTGTGCAGGTGTCTCTCAAAAATTGGCAGAAAGTGGT	509
Qy	421	GAGAAATCCGATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT	480
Dd	510	GAGAAATCCGATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT	569
Qy	481	GCACTGGGCATTATAATGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCATT	540
Dd	570	GCACTGGGCATTATAATGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCATT	629
Qy	541	GATGCAAAATATGGTGGAGGAACAGCATATTTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	600
Dd	630	GATGCAAAATATGGTGGAGGAACAGCATATTTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	689
Qy	601	TCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACTTTCTAT	660
Dd	690	TCGAGTCTGTGGGAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACTTTCTAT	749
Qy	661	ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC	720
Dd	750	ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC	809
Qy	721	TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780
Dd	810	TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	869
Qy	781	ATCGATGATTGGCCAGAATGAAGAAGATTTCAGATGTATTTGCAAGAGACGAAG	840
Dd	870	ATGGATGATTGGCCAGAATGAAGAAGATTTCAGATGTATTTGCAAGAGACGAAG	929
Qy	841	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT	900
Dd	930	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT	989
Qy	901	GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG	960
Dd	990	GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG	1049
Qy	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTC	1020
Dd	1050	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTC	1109
Qy	1021	AAAAGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC	1080
Dd	1110	AAAAGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC	1169
Qy	1081	CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCAATTGAAAAGTAATAAGG	1132
Dd	1170	CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCAATTGAAAAGTAATAAGG	1221

RESULT 8
ADB75195
ID ADB75195 standard; cDNA; 3654 BP.
XX
AC ADB75195;
XX

DT	04-DEC-2003	(first entry)
XX	Prostate cancer marker cDNA.	
DE	Prostate; cancer; cytostatic; gene therapy; marker; ss.	
XX	Homo sapiens.	
XX	WO2003009814-A2.	
XX	06-FEB-2003.	
XX	25-JUL-2002; 2002WO-US023913.	
XX	25-JUL-2001; 2001US-0307982P.	
PR	22-AUG-2001; 2001US-0314356P.	
PR	25-SEP-2001; 2001US-0325020P.	
PR	12-DEC-2001; 2001US-0341746P.	
PR	05-MAR-2002; 2002US-0362158P.	
XX	(MILL-) MILLENNIUM PHARM INC.	
PA	Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;	
XX	Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;	
XX	WPI; 2003-248033/24.	
DR	New nucleic acid molecule, useful for diagnosing or treating prostate	
XX	cancer.	
PS	Claim 1; SEQ ID NO 19; 99pp; English.	
XX	The invention relates to newly discovered cancer markers associated with	
CC	the cancerous state of prostate cells. Also disclosed is a method of	
CC	assessing whether a patient is afflicted with prostate cancer. The method	
CC	of the invention involves assessing whether a patient is afflicted with	
CC	prostate cancer by comparing the level of expression of a marker in a	
CC	patient sample and the normal level of expression of the marker in a	
CC	control non-prostate cancer sample, where a significant increase in the	
CC	level of expression of the marker in the patient sample and the normal	
CC	level indicates that the patient is afflicted with prostate cancer.	
CC	Nucleic acids of the invention are useful for diagnosing or treating	
CC	prostate cancer, and may be useful in gene therapy. Sequences given in	
CC	ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence	
CC	data for this patent did not form part of the printed specification, but	
CC	was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX	Sequence 3654 BP; 1050 A; 751 C; 888 G; 965 T; 0 U; 0 Other;	
SQ	Query Match 98.8%; Score 1132; DB 10; Length 3654;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCGGGCTTCTGT 60	
Db		
Db	90 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCGGGCTTCTGT 149	
QY	61 GCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGGTACGCTGGACCGCGCTCCCGC 120	
Db		
Db	150 GCTATGGTCTCTGGCTGACTTCGGGGCGCGTGTGGTACGCTGGACCGCGCTCCCGC 209	
QY	121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGG 180	
Db		
Db	210 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGG 269	
QY	181 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240	
Db		
Db	270 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 329	
QY	241 CGCCGCGGTGTCTATGGAGAAATCTCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 300	
Db		
Db	330 CGCCGCGGTGTCTATGGAGAAATCTCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATCCA 389	

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db |||||
QY 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 449
Db |||||
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT 420
Db |||||
QY 450 GGCCACGATATCAACTATTTGGCTTTGTGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGT 509
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGGTGGTGGTGGCTTATGTGT 480
Db |||||
QY 510 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGGTGGTGGTGGCTTATGTGT 569
QY 481 GCACTGGGCATTATAATGGCTCTTTTGTACCGCACACGCACTGGCAAGGTCAGGTCAATT 540
Db |||||
QY 570 GCACTGGGCATTATAATGGCTCTTTTGTACCGCACACGCACTGGCAAGGTCAGGTCAATT 629
QY 541 GATCAAAATATGTTGGAAGGAAGACAGCATATTTTAAGTTCTTTTCTGTGGAATACTCAGAAA 600
Db |||||
QY 630 GATCAAAATATGTTGGAAGGAAGACAGCATATTTTAAGTTCTTTTCTGTGGAATACTCAGAAA 689
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db |||||
QY 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 749
QY 661 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db |||||
QY 750 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 809
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGTATGAACCTCCCAATCAGATGAGC 780
Db |||||
QY 810 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGTATGAACCTCCCAATCAGATGAGC 869
QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 840
Db |||||
QY 870 ATGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 929
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db |||||
QY 930 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 989
QY 901 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG 960
Db |||||
QY 990 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGCTCGTTTATCACCAGTGAGGAG 1049
QY 961 CAGGAGCTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1020
Db |||||
QY 1050 CAGGAGCTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC 1080
Db |||||
QY 1110 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGC 1169
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTGAAAGTAATAAGG 1132
Db |||||
QY 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTGAAAGTAATAAGG 1221

RESULT 9

ADB75201

ID ADB75201 standard; cDNA; 2069 BP.

XX AC ADB75201;

XX AC ADB75201;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

OS Homo sapiens.

XX Homo sapiens.

PN WO2003009814-A2.

XX 06-FEB-2003.
PD
XX
PF 25-JUL-2002; 2002WO-US023913.
XX
PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR WPI; 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
PT
XX
PS Claim 1; SEQ ID NO 25; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2069 BP; 554 A; 439 C; 528 G; 548 T; 0 U; 0 Other;

Query Match 95.5%; Score 1095; DB 10; Length 2069;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCGGCCCTGGCCCGGCGCTTCTGT 60
Db |||||
QY 90 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCGGCCCTGGCCCGGCGCTTCTGT 149
QY 61 GCTATGGTCTCTGGTGAATTCGGGGCGCGTGTGTTACCGCTGGACCGGCGGCTCCGC 120
Db |||||
QY 150 GCTATGGTCTCTGGTGAATTCGGGGCGCGTGTGTTACCGCTGGACCGGCGGCTCCGC 209
QY 121 TACGACGTGAGCCGCTTGGGCCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 180
Db |||||
QY 210 TACGACGTGAGCCGCTTGGGCCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCG 269
QY 181 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240
Db |||||
QY 270 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 329
QY 241 CGCCCGGCTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCA 300
Db |||||
QY 330 CGCCCGGCTGTCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCA 389
QY 301 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db |||||
QY 390 AGGCTTATTTATGCCAGCTGAGTGGATTTGGCAGTCAGGAAGCTTCTGCCGGTTAGCT 449
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGTCAGGTGTCTCTCAAAAATTGGCAGAAAGTGGT 420
Db |||||
QY 450 GGCCACGATATCAACTATTTGGCTTTGTGTCAGGTGTCTCTCAAAAATTGGCAGAAAGTGGT 509

QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480
|||||
Db 510 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 569
|||||
QY 481 GCACTGGGCATTATAATGGCTCTTTTACCCGCACACGCACCTGGCAAGGTCAGGTCATT 540
|||||
Db 570 GCACTGGGCATTATAATGGCTCTTTTACCCGCACACGCACCTGACAAGGTCAGGTCATT 629
|||||
QY 541 GATGCAAAATATGGTGGAGAAACAGCATATTTAAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
|||||
Db 630 GATGCAAAATATGGTGGAGAAACAGCATATTTAAAGTTCTTTTCTGTGGAAAACTCAGAAA 689
|||||
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
|||||
Db 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 749
|||||
QY 661 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTTC 720
|||||
Db 750 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTTC 809
|||||
QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
|||||
Db 810 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 869
|||||
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAGAAGACGAAG 840
|||||
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAGAAGACGAAG 929
|||||
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 900
|||||
Db 930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 989
|||||
QY 901 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 960
|||||
Db 990 GAGGAGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 1049
|||||
QY 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTATAACACCCCAAGCTTCTTTT 1020
|||||
Db 1050 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTATAACACCCCAAGCTTCTTTT 1109
|||||
QY 1021 AAAAGGATCCTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAAATTTGGATTCAGC 1080
|||||
Db 1110 AAAAGGATCCTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAAATTTGGATTCAGC 1169
|||||
QY 1081 CGCGAAGAGATTTATCAGTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAGCT 1140
|||||
Db 1170 CGCGAAGAGATTTATCAGTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAGCT 1229
|||||
QY 1141 AGTCTC 1146
|||||
Db 1230 AGTCTC 1235

RESULT 10
ADB75203
ID ADB75203 standard; cDNA; 2626 BP.

AC ADB75203;

DT 04-DEC-2003 (first entry)

XX Prostate cancer marker cDNA.

DE Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

OS WO2003009814-A2.

XX 06-FEB-2003.

PD 25-JUL-2002; 2002WO-US023913.

XX

PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR WPI; 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
PT
XX
PS Claim 1; SEQ ID NO 27; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 2626 BP; 697 A; 573 C; 664 G; 692 T; 0 U; 0 Other;

Query Match 94.3%; Score 1081; DB 10; Length 2626;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCGATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCGGCGCTTCTGT 60
|||||
Db 90 ATGGCACTGCAGGCGATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCGGCGCTTCTGT 149
|||||
QY 61 GCTATGGTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTCCCGC 120
|||||
Db 150 GCTATGGTCTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTCCCGC 209
|||||
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 180
|||||
Db 210 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 269
|||||
QY 181 CGGGAGCGCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240
|||||
Db 270 CGGGAGCGCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 329
|||||
QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA 300
|||||
Db 330 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA 389
|||||
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCAGTCAGGAAGCTTCTGCCGTTAGCT 360
|||||
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCAGTCAGGAAGCTTCTGCCGTTAGCT 449
|||||
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAGTGGT 420
|||||
Db 450 GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAGTGGT 509
|||||
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCCTTATGTGT 480
|||||
Db 510 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCCTTATGTGT 569
|||||
QY 481 GCACCTGGGCATTATAATGGCTCTTTTGTACCGCACACGCACTGGCAAGGTCAGGTCATT 540

|||||
Db 570 GCACTGGGCATTATAATGGCTCTTTTGGCCGCACACGCACTGACAAGGTCAGGTCATT 629
QY 541 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAAGTCTCTTTTGTGGAAAACTCAGAAA 600
Db 630 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAAGTCTCTTTTGTGGAAAACTCAGAAA 689
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 749
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCACTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCACTTC 809
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 869
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAAGAACGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAAGAACGAAG 929
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAATCTTTGACGGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 989
QY 901 GAGGAGTGTTCATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 990 GAGGAGTGTTCATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATCAGC 1080
Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATCAGC 1169
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTTGAAAAGTAATAAG 1132
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTTGAAAAGTAATAAG 1221

RESULT 11

AAV58584
ID AAV58584 standard; cDNA; 1621 BP.
XX AC AAV58584;
XX 25-MAR-2003 (revised)
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone F1-12.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 5..1153
FT /*tag= a
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US003690.
XX
PR 25-FEB-1997; 97US-00806596.
PR 01-AUG-1997; 97US-00904809.
PR 09-FEB-1998; 98US-00020747.

XX (CORI-) CORIXA CORP.
PA
XX
PI Xu J, Dillon DC;
XX
DR WPI; 1998-480805/41.
DR P-PSDB; AAW69383.
XX
PT Novel human prostate specific tumour protein and fragments - useful for
PT detecting and treating prostate cancers.
XX
PS Claim 1; Page 81-82; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may also
CC be conjugated to a therapeutic agent for use in therapy of prostate
CC cancers. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;
Query Match 93.4%; Score 1070; DB 2; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGTCCGGCCTGGCCCCCGGCCCTCTGCTGCTATGCTCCTGGCTGACTTCGGGG 85
Db 30 TGGAGCTGTCCGGCCTGGCCCCCGGCCCTCTGCTGCTATGCTCCTGGCTGACTTCGGGG 89
QY 86 CGCGTGTGTACGCGTGGACCGGCCCGGCCCTCCCGTACGACGTGAGCCGCTTGGGCCGGG 145
Db 90 CGCGTGTGTACGCGTGGACCGGCCCGGCCCTCCCGTACGACGTGAGCCGCTTGGGCCGGG 149
QY 146 GCAAGCGCTCGTGTGCTGACCTGAAAGCAGCGCGGGAGCCCGCTGCTGCGGCGTC 205
Db 150 GCAAGCGCTCGTGTGCTGACCTGAAAGCAGCGCGGGAGCCCGCTGCTGCGGCGTC 209
QY 206 TGTGAAGCGGTGCGATGTGCTGTGAGCCCTTCGCGCGGCTCATGGAAGAACTCC 265
Db 210 TGTGAAGCGGTGCGATGTGCTGTGAGCCCTTCGCGCGGCTCATGGAAGAACTCC 269
QY 266 AGCTGGGCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329
QY 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGTGGCCACGATATCAACTATTTGGCTT 385
Db 330 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGTGGCCACGATATCAACTATTTGGCTT 389
QY 386 TGTGAGGTGTTCTCTCAAAAATTTGGCAGAAGTGTGAGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAAATTTGGCAGAAGTGTGAGAATCCGTATGCCCGCTGAATC 449
QY 446 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGCACTGGGCATTATAATGGCTCTTT 505
Db 450 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGCACTGGGCATTATAATGGCTCTTT 509
QY 506 TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG 565
Db 510 TTGACCGCACACGCACTGACAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG 569
QY 566 CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAGCACCTCGAG 625
Db 570 CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAGCACCTCGAG 629
QY 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGAGATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGAGATGGGG 689

XX Homo sapiens.
OS WO200151633-A2.
XX
PN 19-JUL-2001.
XX
PD 16-JAN-2001; 2001WO-US001574.
XX
PF 14-JAN-2000; 2000US-00483672.
XX
PR (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 262-263; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

Query Match 93.4%; Score 1070; DB 4; Length 1621;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 TGAGAGTGTCCGGCCTGGCCCGGCCCGCTTCTGTGCTATGGTCTCGGCTGACCTCGGGG 85
Db 30 TGAGAGTGTCCGGCCTGGCCCGGCCCGCTTCTGTGCTATGGTCTCGGCTGACCTCGGGG 89

Qy 86 CGCGTGTGGTACGCGTGGACCGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGSCCGG 145
Db 90 CGCGTGTGGTACGCGTGGACCGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGSCCGG 149

Qy 146 GCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGGCGGCTC 205
Db 150 GCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGGGGAGCCCGCTGCTGGCGGCTC 209

Qy 206 TGTGCAAGCGGTGGATGTGCTGGAGCCCTTCCGCCCGGCTGTCATGGAGAACTCC 265
Db 210 TGTGCAAGCGGTGGATGTGCTGGAGCCCTTCCGCCCGGCTGTCATGGAGAACTCC 269

Qy 266 AGCTGGGCCAGAGATTCTGCAGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 325
Db 270 AGCTGGGCCAGAGATTCTGCAGCGGGAATAATCCAAAGCTTATTTATGCCAGGCTGAGTG 329

Qy 326 GATTGGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 385
Db 330 GATTGGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTT 389

Qy 386 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGTATGCCCGCTGAATC 445
Db 390 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGTATGCCCGCTGAATC 449

Qy 446 TCCTGGCTGACCTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTATATGGCTCTTT 505
Db 450 TCCTGGCTGACCTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTATATGGCTCTTT 509

Qy 506 TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAATATGGTGAAGGAACAG 565
Db 510 TTGACCGCACACGCACTGCAAGGGTCAGGTCAATTGATGCAATATGGTGAAGGAACAG 569

Qy 566 CATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db 570 CATATTTAAGTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629

Qy 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685
Db 630 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689

Qy 686 AATTCATGGCTGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAGGACTTG 745
Db 690 AATTCATGGCTGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAGGACTTG 749

Qy 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805
Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 809

Qy 806 AGAAGTTTGCAGATGTATTGCAAGAAGACGAGGAGGAGTGGTGTCAAATCTTTGACG 865
Db 810 AGAAGTTTGCAGATGTATTGCAAGAAGACGAGGAGGAGTGGTGTCAAATCTTTGACG 869

Qy 866 GCACAGATGCTGTGACTCCGGTTCTGACTTTTGGAGGAGTGTTCATCATGATCACA 925
Db 870 GCACAGATGCTGTGACTCCGGTTCTGACTTTTGGAGGAGTGTTCATCATGATCACA 929

Qy 926 ACAAGGAACGGGGCTGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCGCCCTGCAC 985
Db 930 ACAAGGAACGGGGCTGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCGCCCTGCAC 989

Qy 986 CTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTTCAAAGGGGATCCTTTCATAGGAGAAC 1045
Db 990 CTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTTCAAAGGGGATCCTTTCATAGGAGAAC 1049

Qy 1046 AACTGAGGAGATACCTTGAAGAATTTGGATTTCAGCCCGGAGAGATTTATCAGCTTAAC 1105
Db 1050 AACTGAGGAGATACCTTGAAGAATTTGGATTTCAGCCCGGAGAGATTTATCAGCTTAAC 1109

Qy 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146
Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

Search completed: July 27, 2005, 05:31:53
Job time : 707 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 02:32:35 ; Search time 5147 Seconds
(without alignments)
10788.746 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcagggcattctc.....ataaqqtaaaagctactctc 1146

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9416466

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

```
Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	1146	100.0	1146	6	AX497154	AX497154 Sequence	
2	1146	100.0	2005	6	AX497152	AX497152 Sequence	
3	1146	100.0	2005	6	AX497161	AX497161 Sequence	
4	1146	100.0	2005	9	AF158378	AF158378 Homo sapi	
5	1146	100.0	2069	6	AX497155	AX497155 Sequence	
6	1132	98.8	3654	6	AX497157	AX497157 Sequence	
7	1070	93.4	1621	6	BD242020	BD242020 Compounds	
8	1070	93.4	1621	6	AR237203	AR237203 Sequence	
9	1070	93.4	1621	6	AR278227	AR278227 Sequence	
10	1070	93.4	1621	6	AR366923	AR366923 Sequence	
11	1070	93.4	1621	6	AR370819	AR370819 Sequence	
12	1070	93.4	1621	6	AR392324	AR392324 Sequence	
13	1070	93.4	1621	6	AR399959	AR399959 Sequence	
14	1070	93.4	1621	6	AR405226	AR405226 Sequence	
15	1070	93.4	1621	6	AR439430	AR439430 Sequence	
16	1070	93.4	1621	6	AR563606	AR563606 Sequence	
17	1070	93.4	1621	6	AX106326	AX106326 Sequence	
18	1070	93.4	1621	6	AX140617	AX140617 Sequence	
19	1070	93.4	1621	6	AX200477	AX200477 Sequence	

20	1070	93.4	1621	6	AX267133	AX267133 Sequence
21	1070	93.4	1621	6	BD070256	BD070256 Compounds
22	1070	93.4	2045	6	CQ726257	CQ726257 Sequence
23	1070	93.4	2376	6	CQ489417	CQ489417 Sequence
24	1070	93.4	2376	6	CQ490005	CQ490005 Sequence
25	1070	93.4	2376	6	CQ493361	CQ493361 Sequence
26	1070	93.4	2376	6	CQ495259	CQ495259 Sequence
27	1019	88.9	1674	6	BD155688	BD155688 Primer fo
28	1019	88.9	1674	6	AX875662	AX875662 Sequence
29	1019	88.9	1674	9	AK000912	AK000912 Homo sapi
30	866	75.6	2041	9	AF047020	AF047020 Homo sapi
31	797	69.5	1294	6	CQ490746	CQ490746 Sequence
32	797	69.5	1294	6	CQ490859	CQ490859 Sequence
33	797	69.5	1294	6	CQ495858	CQ495858 Sequence
34	797	69.5	1294	6	CQ496588	CQ496588 Sequence
35	797	69.5	1294	6	CQ496690	CQ496690 Sequence
36	756	66.0	1039	6	AX593026	AX593026 Sequence
37	672	58.6	858	9	AY330489	AY330489 Homo sapi
38	613	53.5	1317	6	BD159629	BD159629 Primer fo
39	613	53.5	1317	6	AX882271	AX882271 Sequence
40	613	53.5	1317	9	AK022765	AK022765 Homo sapi
41	595	51.9	2946	9	BC009471	BC009471 Homo sapi
42	595	51.9	3023	6	AX497159	AX497159 Sequence
43	524	45.7	720	6	BD145333	BD145333 Primer fo
44	524	45.7	720	6	AX865271	AX865271 Sequence
45	493	43.0	865	6	CQ488657	CQ488657 Sequence

ALIGNMENTS

```

RESULT 1
AX497154
LOCUS AX497154 1146 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from Patent WO0227324.
ACCESSION AX497154
VERSION AX497154.1 GI:23342546
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Richardson,J.
AUTHORS Alpha-methylacyl-coa racemase in prostate cancers
TITLE Patent: WO 0227324-A 3 04-APR-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
    Location/Qualifiers
    1..1146
       /organism="Homo sapiens"
       /mol_type="unassigned DNA"
       /db_xref="taxon:9606"
source

```

ORIGIN

Query Match	100.0%;	Score 1146;	DB 6;	Length 1146;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1146:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:

QY 1 ATGGCACTGACAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCCGGGCCCCGTTCTGT 60
|||||
db 1 ATGGCACTGACAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCCGGGCCCCGTTCTGT 60

QY	61	GCTATGGTCTCGGTGACTTCGGGGCGCGTGTGGTACGCTGGACCGCGCGGCTCCCGC	120
Db			
QY	61	GCTATGGTCTCGGTGACTTCGGGGCGCGTGTGGTACGCTGGACCGCGCGGCTCCCGC	120
Db			
QY	121	TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGTCGTAGTGTGGACCTGAAGCAGCCG	180
Db			
QY	121	TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGTCGTAGTGTGGACCTGAAGCAGCCG	180
Db			
QY	181	CGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC	240
Db			
QY	181	CGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC	240
Db			
QY	241	CGCCGGGTGTATGAGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA	300
Db			
QY	241	CGCCGGGTGTATGAGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA	300
Db			
QY	301	AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360
Db			
QY	301	AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360
Db			
QY	361	GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGSCAGAAGTGGT	420
Db			
QY	361	GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGSCAGAAGTGGT	420
Db			
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGTGGCTTATGTGT	480
Db			
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGTGGCTTATGTGT	480
Db			
QY	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACGCACTGGCAAGGTCAGGTCATT	540
Db			
QY	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACGCACTGGCAAGGTCAGGTCATT	540
Db			
QY	541	GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAGAACTCAGAA	600
Db			
QY	541	GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAGAACTCAGAA	600
Db			
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT	660
Db			
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT	660
Db			
QY	661	ACGACTTACAGGACAGCAGATGGGGAATTCATGGTGTGGAGCAATAGAACCCAGTTC	720
Db			
QY	661	ACGACTTACAGGACAGCAGATGGGGAATTCATGGTGTGGAGCAATAGAACCCAGTTC	720
Db			
QY	721	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780
Db			
QY	721	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780
Db			
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGCAAGAAAGACGAAG	840
Db			
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGCAAGAAAGACGAAG	840
Db			
QY	841	GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT	900
Db			
QY	841	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCGTGTGACTCCGGTTCGACTTTT	900
Db			
QY	901	GAGGAGGTTGTTTCATCATGATCAAAAGGAACGGGCTCGTTTATCACCAGTGAGGAG	960
Db			
QY	901	GAGGAGGTTGTTTCATCATGATCAAAAGGAACGGGCTCGTTTATCACCAGTGAGGAG	960
Db			
QY	961	CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTTC	1020
Db			
QY	961	CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTCTTTTC	1020
Db			
QY	1021	AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1080
Db			
QY	1021	AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1080
Db			
QY	1081	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCAATGAAAGTAATAAGGTAAGACT	1140
Db			
QY	1081	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCAATGAAAGTAATAAGGTAAGACT	1140
Db			

QY	1141	AGTCTC	1146
Db			
QY	1141	AGTCTC	1146
Db			
RESULT 2			
LOCUS	AX497152	2005 bp	DNA
DEFINITION	Sequence 1 from Patent WO227324.		linear
ACCESSION	AX497152		
VERSION	AX497152.1	GI:23342545	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Richardson,J.		
TITLE	Alpha-methylacyl-coa racemase in prostate cancers		
JOURNAL	Patent: WO 0227324-A 1 04-APR-2002;		
FEATURES	Millennium Pharmaceuticals, Inc. (US)		
source	Location/Qualifiers		
	1. .2005		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
	Query Match	100.0%;	Score 1146; DB 6; Length 2005;
	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 1146; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	1	ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGT	60
Db			
QY	66	ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCCCGTTCTGT	125
Db			
QY	61	GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGCTCCCGC	120
Db			
QY	126	GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGCTCCCGC	185
Db			
QY	121	TACGACGTGAGCCGCTTGGCCGGGGCAAGCGCTCGTAGTGTGCTGGAGCCCTTC	180
Db			
QY	186	TACGACGTGAGCCGCTTGGCCGGGGCAAGCGCTCGTAGTGTGCTGGACCTGAAGCAGCCG	245
Db			
QY	181	CGGGAGCCCGCTGCTCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC	240
Db			
QY	246	CGGGAGCCCGCTGCTCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC	305
Db			
QY	241	CGCCCGGTGTATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATAATCCA	300
Db			
QY	306	CGCCCGGTGTATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGGAATAATCCA	365
Db			
QY	301	AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360
Db			
QY	366	AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	425
Db			
QY	361	GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAAATTTGGCAGAGTGGT	420
Db			
QY	426	GGCCACGATATCAACTATTGGCTTTGTGAGTGTCTCTCAAAAAATTTGGCAGAGTGGT	485
Db			
QY	421	GAGAATCCGTATGCCCGCTGAATCTCCTGCTGACTTTGCTGGTGGCTTATGTGT	480
Db			
QY	486	GAGAATCCGTATGCCCGCTGAATCTCCTGCTGACTTTGCTGGTGGCTTATGTGT	545
Db			
QY	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	540
Db			
QY	546	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCATT	605
Db			
QY	541	GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAGAACTCAGAAA	600
Db			
QY	606	GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTCTGTGGAAGAACTCAGAAA	665
Db			
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT	660
Db			

Db 666 TCGAGTCTGTGGGAGCACCTCGAGGACAGAACATGTTGGATGGTGAGCACCTTTCTAT 725
QY 661 ACAGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCACTTC 720
Db 726 ACAGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCCACTTC 785
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGTAGTAACTTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGTAGTAACTTCCCAATCAGATGAGC 845
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTTGCAAGAAGACGAAG 840
Db 846 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTTGCAAGAAGACGAAG 905
QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 906 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 965
QY 901 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 960
Db 966 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 1025
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTCAGC 1080
Db 1086 AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTCAGC 1145
QY 1081 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGTTAAAGCT 1140
Db 1146 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAAAGTTAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 3
AX497161
LOCUS AX497161 2005 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent WO0227324.
ACCESSION AX497161
VERSION AX497161.1 GI:23342554
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Richardson, J.
TITLE Alpha-methylacyl-coA racemase in prostate cancers
JOURNAL Patent: WO 0227324-A 10 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..2005
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
66..1214
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD48647.1"
/db_xref="GI:23342555"
/translation="MALQGISVVELSGLAPGPFAMVLADFGARVVRVDRPGSRDYDS
RLGRKRSVLDLKQPRGAALVRLRCKRSDVLLLEPFRRGVMEKQLGPEILQRENPR
IYARLSGFGSGSPCRLAGHDINYLALSGVLISKIRSGENPYAPLNLLADFAGGLMC
ALGIIMALFDRFTGKQVIDANMVEGTAYLSFLWKTQKSLWEAPRGQNMLDGGAP
FYTTYRTADGEFMAVGAIEPQFYELLIKGLKSLDELPNQMSMDWPFEMKKKFDVFA
KKTKAECQIFDGTDACTVPLTFFBVBVHHDNKRGFSITSEODVSPRPAPLLNT
PAIPSKRDPFIGEHTTEILEEFGFSREEIYQLNSDKIIESNKVKASL"

ORIGIN
Query Match 100.0%; Score 1146; DB 6; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches - 0; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGCCTGGCCCCGGGCCCGTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGCCTGGCCCCGGGCCCGTCTGT 125
QY 61 GCTATGGTCTGTGGTGAATTCGGGGCGCGTGTGTACCGCTGGACCGCGCCCGTCCCGC 120
Db 126 GCTATGGTCTGTGGTGAATTCGGGGCGCGTGTGTACCGCTGGACCGCGCCCGTCCCGC 185
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGTCTGTGCAAGCGGTCTGGATGTGCTGCTGGAGCCCTTC 240
Db 186 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGTCTGTGCAAGCGGTCTGGATGTGCTGCTGGAGCCCTTC 245
QY 181 CGGGAGCGCCGCTGCTGCGGCGTCTGTGCAAGCGGTCTGGATGTGCTGCTGGAGCCCTTC 240
Db 246 CGGGAGCGCCGCTGCTGCGGCGTCTGTGCAAGCGGTCTGGATGTGCTGCTGGAGCCCTTC 305
QY 241 CGCCCGGCTGTATGAGAGAAATCCAGCTGGGCCACAGAGATTTCTGACGGGGAAATCCA 300
Db 306 CGCCCGGCTGTATGAGAGAAATCCAGCTGGGCCACAGAGATTTCTGACGGGGAAATCCA 365
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 366 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTTCAGGAAGCTTCTGCCGGTTAGCT 425
QY 361 GGCCACGATATCACTAATTTGGCTTTGTGAGGTGTTCTCTCAAAAAATGGCAGAAAGTGT 420
Db 426 GGCCACGATATCACTAATTTGGCTTTGTGAGGTGTTCTCTCAAAAAATGGCAGAAAGTGT 485
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTTGT 480
Db 486 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTTGT 545
QY 481 GCACTGGGCATTTATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGTCATT 540
Db 546 GCACTGGGCATTTATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGTCATT 605
QY 541 GATCAAAATATGTTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 600
Db 606 GATCAAAATATGTTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA 665
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATTCATGCTGTTGGATGGTGGACCTTCTAT 660
Db 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATTCATGCTGTTGGATGGTGGACCTTCTAT 725
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTC 720
Db 726 ACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCCACTTC 785
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTTGCAAGAAGACGAAG 840
Db 846 ATGATGATTTGGCCAGAAATGAAGAAGAGTTTGCAGATGATTTGCAAGAAGACGAAG 905
QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 906 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 965
QY 901 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 960
Db 966 GAGGAGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 1025
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085

QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1080
|||||
Db 1086 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1145
|||||
QY 1081 CGCGAAGAGATTTATCAGTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1140
|||||
Db 1146 CGCGAAGAGATTTATCAGTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1205
|||||
QY 1141 AGTCTC 1146
|||||
Db 1206 AGTCTC 1211

RESULT 4
AF158378
LOCUS AF158378 2005 bp mRNA linear PRI 11-FEB-2000
DEFINITION Homo sapiens alpha-methylacyl-CoA racemase (RM) mRNA, complete cds.
ACCESSION AF158378
VERSION AF158378.1 GI:6653127
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2005)
AUTHORS Ferdinandusse,S., Denis,S., Clayton,P.T., Graham,A., Rees,J.E.,
Allen,J.T., McLean,B.N., Brown,A.Y., Vreken,P., Waterham,H.R. and
Wanders,R.J.
TITLE Mutations in the gene encoding peroxisomal alpha-methylacyl-CoA
racemase cause adult-onset sensory motor neuropathy
JOURNAL Nat. Genet. 24 (2), 188-191 (2000)
MEDLINE 20120722
PUBMED 10655068
REFERENCE 2 (bases 1 to 2005)
AUTHORS Ferdinandusse,S., Denis,S. and Wanders,R.J.A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1999) Clinical Chemistry, Academic Medical
Center, Meibergdreef 9, Amsterdam 1105 AZ, The Netherlands
FEATURES
source
1..2005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="skin fibroblast"
1..2005
/gene="RM"
66..1214
/gene="RM"
/function="racemisation of stereoisomers of
2-methyl-branched chain fatty acyl-CoA esters"
/codon_start=1
/product="alpha-methylacyl-CoA racemase"
/protein_id="AAF22610.1"
/db_xref="GI:6653128"
/translation="MALQGISVVELSGLAPGPFCAVLADFGARVVRVDRPGSRDVS
RLGRKRSVLVLKQPRGAAVLRRLCKRSDVLLLEPFRRGVMEKQLQGLPEILQRENPLR
IYARLSGFGQSGFRCRLAGHDINYLALSGVLSKIGRSGENPYAPLNLLADFAGGGLMC
ALGIIMALFDRITGKGQVIDANMVEGTAYLSSFLWKTKSSLWEAPRQNMLDGGAP
FYTTYRTADGEFMAVGAIEPQFYELLIKGLKSDLELPNQMSMDDPWMKKKFAADVFA
KXTKAEWCQIFDGTDACVTPVLTFFEEVVHHDHNGKRSFITSEEQDVSPPRAPLLNLT
PAIPSFKRDPFIGEHTTEIILEEFGFSREBIYQLNSDKIIESNKKVASL"
90
/gene="RM"
/replace="a"
589
variation
/gene="RM"
/replace="a"
667
variation
/gene="RM"
/replace="t"
783
variation
/gene="RM"

variation /replace="t"
894
/gene="RM"
/replace="g"
ORIGIN
Query Match 100.0%; Score 1146; DB 9; Length 2005;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCGTGT 60
|||||
Db 66 ATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCGTGT 125
|||||
QY 61 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGAGCCGCGCTCCCGC 120
|||||
Db 126 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGAGCCGCGCTCCCGC 185
|||||
QY 121 TACGACGTGAGCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 180
|||||
Db 186 TACGACGTGAGCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCG 245
|||||
QY 181 CGGGAGCGCGCTGCTCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240
|||||
Db 246 CGGGAGCGCGCTGCTCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 305
|||||
QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGSCCCAGAGATTCTGCAGCGGGAATAATCCA 300
|||||
Db 306 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGSCCCAGAGATTCTGCAGCGGGAATAATCCA 365
|||||
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
|||||
Db 366 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425
|||||
QY 361 GGCCACGATATCAACTATTTGGCTTTGTAGTGTTCTCAAAAAATTTGGCAGAAGTGGT 420
|||||
Db 426 GGCCACGATATCAACTATTTGGCTTTGTAGTGTTCTCAAAAAATTTGGCAGAAGTGGT 485
|||||
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCCTTATGTGT 480
|||||
Db 486 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCCTTATGTGT 545
|||||
QY 481 GCACCTGGGCATTATAATGGCTCTTTTGTACCGCACACGCACCTGGCAAGGGTCAGGTCAAT 540
|||||
Db 546 GCACCTGGGCATTATAATGGCTCTTTTGTACCGCACACGCACCTGGCAAGGGTCAGGTCAAT 605
|||||
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
|||||
Db 606 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 665
|||||
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 660
|||||
Db 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 725
|||||
QY 661 ACGACTTACAGGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
|||||
Db 726 ACGACTTACAGGACAGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785
|||||
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
|||||
Db 786 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
|||||
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTTCAGATGTATTTGCAAAAGAACGGAAG 840
|||||
Db 846 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTTCAGATGTATTTGCAAAAGAACGGAAG 905
|||||
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCGACTTTT 900
|||||
Db 906 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCGACTTTT 965
|||||
QY 901 GAGGAGGTTGTTTCATCATGATCAACAAGAACGGGGCTCGTTTATCACCAGTGAAGGAG 960
|||||
Db 966 GAGGAGGTTGTTTCATCATGATCAACAAGAACGGGGCTCGTTTATCACCAGTGAAGGAG 1025
|||||

Qy 961 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
Qy 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTGAGC 1080
Db 1086 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTGAGC 1145
Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAAATAAGGTAAAGCT 1140
Db 1146 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAAATAAGGTAAAGCT 1205
Qy 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 5
AX497155
LOCUS AX497155 2069 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 4 from Patent WO0227324.
ACCESSION AX497155
VERSION AX497155.1 GI:23342548

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Richardson,J.
TITLE Alpha-methylacyl-coa racemase in prostate cancers
JOURNAL Patent: WO 0227324-A 4 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..2069
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
90..1238
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD48644.1"
/db_xref="GI:23342549"
/translation="MALQGISWVELSGLAPPFCAVMVLDFGARVVRVDRPGSRDYDVS
RLRGKRSVLVDLKPFGAAVLRLCKRSDVLEFFRRGVMEKLQLGPEILQRENPR
IYARLSGFGSGSFCRLAGHDINYLALSGVLSKIGRSGENPYAPLNLLADPAGGLMC
ALGIIMALFDRTRTGKQVIDANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAP
FYTYRTADGEFMAVGAIEPQFYELLIKGLKSDLPNQMSMDWDWPEMKKFPADVFA
KKTAEWCQIFDGTDACTPVLTFEEVVDHDKRGSGFITSEEDVSPRPAPLLLNT
PAIPSKRDPFIGEHTHEILEEFGFSREEIYQLNSDKIIESNKVKASL"

CDS
Query Match 100.0%; Score 1146; DB 6; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCACTGCAGGCATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCCGGCGCTTCTGT 60
Db 90 ATGGCACTGCAGGCATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCCGGCGCTTCTGT 149
Qy 61 GCTATGGTCTGGTGACTTCGGGGCGCGTGTGGTACGGGTGGACCGGCGCGCTCCCGC 120
Db 150 GCTATGGTCTGGTGACTTCGGGGCGCGTGTGGTACGGGTGGACCGGCGCGCTCCCGC 209

ORIGIN
Qy 121 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGG 180
Db 210 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCGG 269
Qy 181 CGGGAGCGCGCGTCTGCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240
Db 270 CGGGAGCGCGCGTCTGCGGCGCTGTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 329

Qy 241 CGCCGCGGTGTATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATAATCCA 300
Db 330 CGCCGCGGTGTATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAATAATCCA 389
Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 360
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGGTTAGCT 449
Qy 361 GGCACAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 420
Db 450 GGCACAGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 509
Qy 421 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTTGTGGTGGTGGCTTATGTGT 480
Db 510 GAGAAATCCGTATGCCCGCTGAATCTCTGGCTGACTTTTGTGGTGGTGGCTTATGTGT 569
Qy 481 GCACCTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
Db 570 GCACCTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 629
Qy 541 GATCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 600
Db 630 GATCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGGAATACTCAGAAA 689
Qy 601 TCGAGTCTGTGGAAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 690 TCGAGTCTGTGGAAAGCACTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 749
Qy 661 ACCACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTTC 809
Qy 721 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 869
Qy 781 ATGGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAGAAGACGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGAAAGTTTGCAGATGTATTTGCAAAGAAGACGAAG 929
Qy 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 989
Qy 901 GAGGAGTGTGTCATCATGATCACAAAGGAACCGGGCTCGTTTATCACCACTGAGGAG 960
Db 990 GAGGAGTGTGTCATCATGATCACAAAGGAACCGGGCTCGTTTATCACCACTGAGGAG 1049
Qy 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1109
Qy 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTGAGC 1080
Db 1110 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTGAGC 1169
Qy 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAAATAAGGTAAAGCT 1140
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATATAAATCATTTGAAGTAAATAAGGTAAAGCT 1229
Qy 1141 AGTCTC 1146
Db 1230 AGTCTC 1235

RESULT 6
AX497157
LOCUS AX497157 3654 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 6 from Patent WO0227324.
ACCESSION AX497157
VERSION AX497157.1 GI:23342550
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Richardson,J.
TITLE	Alpha-methylacyl-coa racemase in prostate cancers
JOURNAL	Patent: WO 0227324-A 6 04-APR-2002; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers
FEATURES	
source	1..3654
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
CDS	90..1274
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CAD48645.1"
	/db_xref="GI:23342551"
	/translation="MALQGISVVELSGLAPGPFCAVLADFGARVVRVDRPGSRDVS RLGRKRSVLVDLKQPRGAAVLRLCKRSDVLEPFRRGVMEKLQLGPEILORENPRLIYARLSGFGSGSFCRLAGHDINYLALSGLSKIGRSGENPYAPLNLADFAGGGLMCALGIIMALFDRTRTGKQVIDANMVEGTAYLSSFLWKTOKSSWEAPRGONMLDGGAPFYTTYRTADGEFMVAGIEPQFYELLIKGLKGLDELPNQMSMDDWPEMKKFPADVFAKKTAEWCQIFDGTDACVTPVLTFFEEVVHHDHKNKERSFITSEQDVSPRPAPLLNTPAIPSKRDPFIQEHTEEILEEFGFSREIYQLNSDKIIESNKAGSKFWILYPTHSNI QK"
ORIGIN	
Query Match	98.8%; Score 1132; DB 6; Length 3654;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1132; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT 60
Db	
QY	90 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCGCTTCTGT 149
Db	
QY	61 GCTATGGTCTCGTGAATTCGGGGCGCGTGTGTGACCGTGGACCGCGCCGCTCCCGC 120
Db	
QY	150 GCTATGGTCTCGTGAATTCGGGGCGCGTGTGTGACCGTGGACCGCGCCGCTCCCGC 209
Db	
QY	121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180
Db	
QY	210 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 269
Db	
QY	181 CGGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGTGGATGTGCTGCTGAGCCCTTC 240
Db	
QY	270 CGGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGTGGATGTGCTGCTGAGCCCTTC 329
Db	
QY	241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAATCCA 300
Db	
QY	330 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAATCCA 389
Db	
QY	301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 360
Db	
QY	390 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCGGTTAGCT 449
Db	
QY	361 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAGTGGT 420
Db	
QY	450 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAGTGGT 509
Db	
QY	421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 480
Db	
QY	510 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 569
Db	
QY	481 GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGTCAGGTCATT 540
Db	
QY	570 GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGTCAGGTCATT 629
Db	
QY	541 GATGCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGGAATACTCAGAAA 600
Db	
QY	630 GATGCAAAATATGGTGGAGGAACAGCATATTTAAGTCTTTTCTGTGGAATACTCAGAAA 689
Db	
QY	601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db	

Db	690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 749
QY	
Db	661 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
QY	
Db	750 ACGACTTACAGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 809
QY	
Db	721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
QY	
Db	810 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 869
QY	
Db	781 ATGGATGATTGGCCAGAAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 840
QY	
Db	870 ATGGATGATTGGCCAGAAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGAAG 929
QY	
Db	841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTCTGACTTTT 900
QY	
Db	930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTCTGACTTTT 989
QY	
Db	901 GAGGAGTTGTTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
QY	
Db	990 GAGGAGTTGTTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049
QY	
Db	961 CAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
QY	
Db	1050 CAGGACGTGAGCCCCCGCCCTGACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1109
QY	
Db	1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1080
QY	
Db	1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1169
QY	
Db	1081 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGG 1132
QY	
Db	1170 CGCGAAGAGATTATCAGCTTAACCTCAGATAAAATCATTTGAAAGTAATAAGG 1221
QY	
RESULT 7	
BD242020	1621 bp DNA linear PAT 17-JUL-2003
LOCUS	BD242020
DEFINITION	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.
ACCESSION	BD242020
VERSION	BD242020.1 GI:33051790
KEYWORDS	JP 2002520054-A/107.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1621)
TITLE	Dillon,D.C., Harlocker,S.L., Yugi,J., Xu,J. and Mitcham,J.L.
JOURNAL	Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use
COMMENT	Patent: JP 2002520054-A 107 09-JUL-2002; CORIXA CORP
	OS Homo sapiens (human)
	PN JP 2002520054-A/107
	PD 09-JUL-2002
	PF 14-JUL-1999 JP 2000560247
	PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR
	23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR
	15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR
	09-APR-1999 US 09/288946
	PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI
	JIANGCHUN XU,
	PI JENNIFER LYNN MITCHAM
	PC C12N15/09,A61K38/00,A61K39/395,C07K14/47,C07K16/30,
	PC C12N5/10,
	PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
	PC A61K37/02,
	PC C12N5/00
	CC Compounds for immunotherapy and diagnosis of prostate cancer
	CC and methods
	CC for their use

FH	Key	Location/Qualifiers
FT	source	1. .1621
FT		/organism='Homo sapiens (human)'
FEATURES	Location/Qualifiers	
source	1. .1621	
	/organism="Homo sapiens"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:9606"	
ORIGIN		
	Query Match	93.4%; Score 1070; DB 6; Length 1621;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 1120; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	26	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTCTATGGTCTGGCTGACTTCGGGG 85
Db	30	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTCTATGGTCTGGCTGACTTCGGGG 89
Qy	86	CGCGTGTGGTACGCGTGAACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCCGG 145
Db	90	CGCGTGTGGTACGCGTGAACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCCGG 149
Qy	146	GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCCGGGAGCCCGCGGTGTCTATGGAGAACTCC 205
Db	150	GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCCGGGAGCCCGCGGTGTCTATGGAGAACTCC 209
Qy	206	TGTGCAAGCGGTCCGATGTGCTGTGGAGCCCTTCCGCGCGGTGTCTATGGAGAACTCC 265
Db	210	TGTGCAAGCGGTCCGATGTGCTGTGGAGCCCTTCCGCGCGGTGTCTATGGAGAACTCC 269
Qy	266	AGCTGGGCCAGAGATTCTGCAGCGGGGAAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325
Db	270	AGCTGGGCCAGAGATTCTGCAGCGGGGAAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329
Qy	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 389
Qy	386	TGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGATGCCCGCTGAATC 445
Db	390	TGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGATGCCCGCTGAATC 449
Qy	446	TCCTGGCTGACTTTGCTGGTGGCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 505
Db	450	TCCTGGCTGACTTTGCTGGTGGCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 509
Qy	506	TTGACCGCACACGCACTGGCAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 565
Db	510	TTGACCGCACACGCACTGACAAAGGTCAGGTCAATGATGCAAAATATGGTGAAGGAACAG 569
Qy	566	CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db	570	CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629
Qy	626	GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685
Db	630	GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689
Qy	686	AATTCATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGTGTGATCAAAGGACTTG 745
Db	690	AATTCATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGTGTGATCAAAGGACTTG 749
Qy	746	GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 805
Db	750	GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA 809
Qy	806	AGAAGTTTGCAGATGTAATTTGCAAAGAAGACGAAGGAGAGTGGTGTCAAATCTTTGACG 865
Db	810	AGAAGTTTGCAGATGTAATTTGCAAAGAAGACGAAGGAGAGTGGTGTCAAATCTTTGACG 869
Qy	866	GCACAGATGCCTGTGACTCCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCACA 925
Db	870	GCACAGATGCCTGTGACTCCGGTCTGACTTTTGGAGGAGTGTTCATCATGATCACA 929

Qy	926	ACAAGGAACGGGGCTCGTTTATCACCAGTGAAGGAGCAGGACGTGAGCCCCCGCTGCAC	985
Db	930	ACAAGGAACGGGGCTCGTTTATCACCAGTGAAGGAGCAGGACGTGAGCCCCCGCTGCAC	989
Qy	986	CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTATAGGAGAAC	1045
Db	990	CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTATAGGAGAAC	1049
Qy	1046	ACACTGAGGAGATACCTGAAGAATTGGATTTCAGCCGCGAAGAGATTTATCAGCTTAACT	1105
Db	1050	ACACTGAGGAGATACCTGAAGAATTGGATTTCAGCCGCGAAGAGATTTATCAGCTTAACT	1109
Qy	1106	CAGATAAAATCATTGAAAGTAATAAGTAAAGCTAGTCTC	1146
Db	1110	CAGATAAAATCATTGAAAGTAATAAGTAAAGCTAGTCTC	1150
RESULT 8			
AR237203			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match 93.4%; Score 1070; DB 6; Length 1621;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	26	TGGAGCTGTCCGGCCTGSCCCCGGCGGCTTCTGTGCTATGGTCTTGGCTGACTTCGGGG	85
Db	30	TGGAGCTGTCCGGCCTGSCCCCGGCGGCTTCTGTGCTATGGTCTTGGCTGACTTCGGGG	89
Qy	86	CGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG	145
Db	90	CGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG	149
Qy	146	GCAAGCGCTCGTATGTGGAACCTGAAGCAGCCGCGGGAGCCCGCTGTCGCGCGTC	205
Db	150	GCAAGCGCTCGTATGTGGAACCTGAAGCAGCCGCGGGAGCCCGCTGTCGCGCGTC	209
Qy	206	TGTGCAAGCGGTCGGATGTGCTGTGGAGCCCTTCCGCGCGGCTTCTATGGAGAACTCC	265
Db	210	TGTGCAAGCGGTCGGATGTGCTGTGGAGCCCTTCCGCGCGGCTTCTATGGAGAACTCC	269
Qy	266	AGCTGGGCCAGAGATTCTGCAGCGGGAATACTCAAGGCTTATTTATGCCAGGCTGAGTG	325
Db	270	AGCTGGGCCAGAGATTCTGCAGCGGGAATACTCAAGGCTTATTTATGCCAGGCTGAGTG	329
Qy	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	385
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	389
Qy	386	TGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGATGCCCGCTGAATC	445
Db	390	TGTCAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAATCCGATGCCCGCTGAATC	449
Qy	446	TCCTGGCTGACTTTGCTGGTGGCTTATGTGCACTGGGCATTATAATGGCTCTTT	505

Db 450 TCCTGGCTGACTTTTGCTGGTGGCGCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 509

QY 506 TTGACCGCACACGCACCTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565

Db 510 TTGACCGCACACGCACCTGACAAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 569

QY 566 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625

Db 570 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629

QY 626 GACAGAAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685

Db 630 GACAGAAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689

QY 686 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745

Db 690 AATTCAATGGCTGTTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749

QY 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 805

Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 809

QY 806 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAAAGSAGAGTGGTGTCAAATCTTTGACG 865

Db 810 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAAAGSAGAGTGGTGTCAAATCTTTGACG 869

QY 866 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 925

Db 870 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 929

QY 926 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCTGCAC 985

Db 930 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCTGCAC 989

QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTCAATAGGAGAAC 1045

Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTCAATAGGAGAAC 1049

QY 1046 AACTGAGGAGATACCTTGAAGAAATTTGGATTGAGTTCAGCCCGGAAGAGATTTTATCAGCTTAACT 1105

Db 1050 AACTGAGGAGATACCTTGAAGAAATTTGGATTGAGTTCAGCCCGGAAGAGATTTTATCAGCTTAACT 1109

QY 1106 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1146

Db 1110 CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC 1150

RESULT 9

AR278227

LOCUS AR278227 1621 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 107 from patent US 6512094.

ACCESSION AR278227

VERSION AR278227.1 GI:29712473

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1621)

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepier,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6512094-A 107 28-JAN-2003;

FEATURES source Location/Qualifiers

1. .1621 /organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 93.4%; Score 1070; DB 6; Length 1621;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 TGGAGCTGTCGGCCTGGCCCCCGGCCCTGTGTCTATGGTCTCTGGCTGACTTCGGGG 85

Db 30 TGGAGCTGTCGGCCTGGCCCCCGGCCCTGTGTCTATGGTCTCTGGCTGACTTCGGGG 89

QY 86 CGCGTGTGTACGCGTGGACCGGCCCGCTCCGCTACGACGTGAGCCGCTTGGGCCCGGG 145

Db 90 CGCGTGTGTACGCGTGGACCGGCCCGCTCCGCTACGACGTGAGCCGCTTGGGCCCGGG 149

QY 146 GCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGCGGGAGCCCGCGTGTCTGCGCGCTC 205

Db 150 GCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCCGCGGGAGCCCGCGTGTCTGCGCGCTC 209

QY 206 TGTCAAGCGGTCGGATGTGCTGTGGAGCCCTTCCGCCCGGTGTCTATGGAGAAACTCC 265

Db 210 TGTCAAGCGGTCGGATGTGCTGTGGAGCCCTTCCGCCCGGTGTCTATGGAGAAACTCC 269

QY 266 AGCTGGGCCACAGATTTCTGCAGCGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 325

Db 270 AGCTGGGCCACAGATTTCTGCAGCGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG 329

QY 326 GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 385

Db 330 GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT 389

QY 386 TGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGTATGCCCGCTGAATC 445

Db 390 TGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGTGAGAAATCCGTATGCCCGCTGAATC 449

QY 446 TCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGTGCACTGGGCATTATATATGGCTCTTT 505

Db 450 TCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGTGCACTGGGCATTATATATGGCTCTTT 509

QY 506 TTGACCGCACACGCACCTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565

Db 510 TTGACCGCACACGCACCTGACAAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 569

QY 566 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625

Db 570 CATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 629

QY 626 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 685

Db 630 GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG 689

QY 686 AATTCATGGCTGTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 745

Db 690 AATTCATGGCTGTGGAGCAATAGAAACCCAGTTCTACGAGCTGCTGATCAAGGACTTG 749

QY 746 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 805

Db 750 GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA 809

QY 806 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAAAGSAGAGTGGTGTCAAATCTTTGACG 865

Db 810 AGAAGTTTGCAGATGTATTTGCAAGAAGACGAAAGSAGAGTGGTGTCAAATCTTTGACG 869

QY 866 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 925

Db 870 GCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGGAGAGGTTGTTTCATCATGATCACA 929

QY 926 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCTGCAC 985

Db 930 ACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCTGCAC 989

QY 986 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTCAATAGGAGAAC 1045

Db 990 CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAGGGATCCTTTCAATAGGAGAAC 1049

QY 1046 AACTGAGGAGATACCTTGAAGAAATTTGGATTGAGTTCAGCCCGGAAGAGATTTTATCAGCTTAACT 1105

Db 1050 AACTGAGGAGATACCTTGAAGAAATTTGGATTGAGTTCAGCCCGGAAGAGATTTTATCAGCTTAACT 1109

QY	206	TGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTCGCCCGCGGTGTCTATGGAGAAACTCC	265
Db	210		
QY	266	AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGCTTATTTATGCCAGGCTGAGTG	325
Db	270	AGCTGGGCCAGAGATTCTGCAGCGGGAATCCAAAGCTTATTTATGCCAGGCTGAGTG	329
QY	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	385
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	389
QY	386	TGTCAGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC	445
Db	390	TGTCAGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC	449
QY	446	TCCTGGCTGACTTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	505
Db	450	TCCTGGCTGACTTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	509
QY	506	TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG	565
Db	510	TTGACCGCACACGCACTGACAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG	569
QY	566	CATATTTAAGTTCCTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	625
Db	570	CATATTTAAGTTCCTTCTGTGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	629
QY	626	GACAGAACATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	685
Db	630	GACAGAACATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	689
QY	686	AATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGTCTGATCAAAAGGACTTG	745
Db	690	AATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGTCTGATCAAAAGGACTTG	749
QY	746	GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGTTGCCAGAAATGAAGA	805
Db	750	GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGTTGCCAGAAATGAAGA	809
QY	806	AGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAAATCTTTGACG	865
Db	810	AGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAAATCTTTGACG	869
QY	866	GCACAGATGCCGTGTGACTCCGGTCTTGACTTTTGAGGAGGTTGTTTCATCATGATCACA	925
Db	870	GCACAGATGCCGTGTGACTCCGGTCTTGACTTTTGAGGAGGTTGTTTCATCATGATCACA	929
QY	926	ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGGACGTGAGCCCCCGCTGCAC	985
Db	930	ACAAGGAACGGGCTCGTTTATCACCAGTGAGGAGGACGTGAGCCCCCGCTGCAC	989
QY	986	CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTCTATAGGAGAAC	1045
Db	990	CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTCTATAGGAGAAC	1049
QY	1046	ACACTGAGGAGATACTTGAAGAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAACT	1105
Db	1050	ACACTGAGGAGATACTTGAAGAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAACT	1109
QY	1106	CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC	1146
Db	1110	CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC	1150

RESULT 12
AR392324
LOCUS AR392324 1621 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 107 from patent US 6613872.
ACCESSION AR392324
VERSION AR392324.1 GI:40116338
KEYWORDS Unknown.

ORGANISM	Unknown.									
REFERENCE	Unclassified.									
AUTHORS	1 (bases 1 to 1621)									
TITLE	Xu,J. and Dillon,D.C.									
JOURNAL	Compounds for immunotherapy of prostate cancer and methods for their use									
FEATURES	Patent: US 6613872-A 107 02-SEP-2003;									
source	Location/Qualifiers									
	1..1621									
	/organism="unknown"									
	/mol_type="genomic DNA"									
ORIGIN										
	Query Match	93.4%;	Score 1070;	DB 6;	Length 1621;					
	Best Local Similarity	99.9%;	Pred. No. 0;							
	Matches 1120;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
QY	26	TGGAGCTGTCCGGCCTGGCCCGGGCCCGCTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	85							
Db	30	TGGAGCTGTCCGGCCTGGCCCGGGCCCGCTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	89							
QY	86	CGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG	145							
Db	90	CGCGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGCTTGGGCCGGG	149							
QY	146	GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCGCGGGAGCCCGCTGTGCGGCGTC	205							
Db	150	GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCGCGGGAGCCCGCTGTGCGGCGTC	209							
QY	206	TGTCAAGCGGTCCGATGTGCTGTGGAGCCCTTCCGCCCGGTGTCTATGGAGAACTCC	265							
Db	210	TGTCAAGCGGTCCGATGTGCTGTGGAGCCCTTCCGCCCGGTGTCTATGGAGAACTCC	269							
QY	266	AGCTGGGCCCCAGAGATTCTGCAGCGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG	325							
Db	270	AGCTGGGCCCCAGAGATTCTGCAGCGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG	329							
QY	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	385							
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	389							
QY	386	TGTCAGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC	445							
Db	390	TGTCAGGTGTTCTCTCAAAATTTGGCAGAAAGTGGTGAGAAATCCGTATGCCCGCTGAATC	449							
QY	446	TCCTGGCTGACTTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	505							
Db	450	TCCTGGCTGACTTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	509							
QY	506	TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG	565							
Db	510	TTGACCGCACACGCACTGACAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG	569							
QY	566	CATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	625							
Db	570	CATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	629							
QY	626	GACAGAACATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	685							
Db	630	GACAGAACATGTTGGATGGTGGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	689							
QY	686	AATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG	745							
Db	690	AATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATCAAAAGGACTTG	749							
QY	746	GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA	805							
Db	750	GACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGATGTTGGCCAGAAATGAAGA	809							
QY	806	AGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAATCTTTGACG	865							
Db	810	AGAAGTTTGCAGATGTATTTGCAAAAGAACGAAAGGCAGAGTGGTGTCAAATCTTTGACG	869							

ORIGIN									
/organism="unknown" /mol_type="genomic DNA"									
Query Match 93.4%; Score 1070; DB 6; Length 1621; Best Local Similarity 99.9%; Pred. No. 0; Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	26	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	85						
Db	30	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	89						
QY	86	CGCGTGTGGTACGCGTGGACCGGCCCCGGCTCCCGCTACGAGTGAGCCGCTTGGGCCGGG	145						
Db	90	CGCGTGTGGTACGCGTGGACCGGCCCCGGCTCCCGCTACGAGTGAGCCGCTTGGGCCGGG	149						
QY	146	GCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGGAGCCGCCGTGCTGCGGCGTC	205						
Db	150	GCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGGAGCCGCCGTGCTGCGGCGTC	209						
QY	206	TGTCAAGCGGTCGGATGTGCTGGAGCCCTCCGCCCGCGGTGTCAATGAGAGAAACTCC	265						
Db	210	TGTCAAGCGGTCGGATGTGCTGGAGCCCTCCGCCCGCGGTGTCAATGAGAGAAACTCC	269						
QY	266	AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG	325						
Db	270	AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTTATGCCAGGCTGAGTG	329						
QY	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	385						
Db	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	389						
QY	386	TGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGTGAGAAATCCGTATGCCCGCTGAATC	445						
Db	390	TGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGTGAGAAATCCGTATGCCCGCTGAATC	449						
QY	446	TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	505						
Db	450	TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	509						
QY	506	TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGTTGGAAGGAACAG	565						
Db	510	TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGTTGGAAGGAACAG	569						
QY	566	CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	625						
Db	570	CATATTTAAGTTCCTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	629						
QY	626	GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG	685						
Db	630	GACAGAACATGTTGGATGGTGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG	689						
QY	686	AATTCAATGGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGCTGATCAAGGACTTG	745						
Db	690	AATTCAATGGCTGTTGGAGCAATAGAACCCCACTTCTACGAGCTGCTGATCAAGGACTTG	749						
QY	746	GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA	805						
Db	750	GACTAAAGTCTGATGAACCTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGA	809						
QY	806	AGAAAGTTTGCAGATGTAATTTGCAAGAAGACGAAAGCAGAGTGGTGCAATCTTTTGACG	865						
Db	810	AGAAAGTTTGCAGATGTAATTTGCAAGAAGACGAAAGCAGAGTGGTGCAATCTTTTGACG	869						
QY	866	GCACAGATGCCTGTGTACTCCGGTCTTGACTTTTGGAGAGGTTGTTTCATCATGATCACA	925						
Db	870	GCACAGATGCCTGTGTACTCCGGTCTTGACTTTTGGAGAGGTTGTTTCATCATGATCACA	929						
QY	926	ACAAAGAACGGGCTCGTTTATCACCAAGTGAAGGAGGACGTGAGCCCCCGCCCTGAC	985						
Db	930	ACAAAGAACGGGCTCGTTTATCACCAAGTGAAGGAGGACGTGAGCCCCCGCCCTGAC	989						
QY	986	CTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTTTCAAAAAGGGATCCTTTTCATAGGAGAAC	1045						

Ddb	990	CTCTGCTGTTAAACACCCAGCCATCCCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAAC	1049	
QY	1046	ACACTGAGGAGATACTTGAAGAATTTGGATTTCAGCCGCGAAGAGATTTATCAGCTTAACT	1105	
Ddb	1050	ACACTGAGGAGATACTTGAAGAATTTGGATTTCAGCCGCGAAGAGATTTATCAGCTTAACT	1109	
QY	1106	CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC	1146	
Ddb	1110	CAGATAAAATCATTTGAAAGTAATAAGGTAAAGCTAGTCTC	1150	
RESULT 15				
AR439430				
LOCUS	AR439430	Sequence 107 from patent US 6664377.	1621 bp	DNA linear PAT 20-FEB-2004
DEFINITION				
ACCESSION	AR439430			
VERSION	AR439430.1	GI:42665339		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1621)			
AUTHORS	Xu,J.			
TITLE	Compounds for immunotherapy of prostate cancer and methods for their use			
JOURNAL	Patent: US 6664377-A 107 16-DEC-2003;			
FEATURES	Location/Qualifiers			
source	1. .1621			
	/organism="unknown"			
	/mol_type="genomic DNA"			
ORIGIN				
Query Match 93.4%; Score 1070; DB 6; Length 1621;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 1120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	26	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	85	
Ddb	30	TGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTGCTATGGTCCCTGGCTGACTTCGGGG	89	
QY	86	CGCGTGTGGTACGCGTGGACCGGCCCCGGCTCCCGCTACGACGTGAGCCGCTTGGSCCGGG	145	
Ddb	90	CGCGTGTGGTACGCGTGGACCGGCCCCGGCTCCCGCTACGACGTGAGCCGCTTGGSCCGGG	149	
QY	146	GCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGGAGCCGCCGTGCTGCGGCGTC	205	
Ddb	150	GCAAGCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGGAGCCGCCGTGCTGCGGCGTC	209	
QY	206	TGTCAAGCGGTCGGATGTGCTGGAGCCCTTCGCCCGCGGTGTCAATGGAGAACTCC	265	
Ddb	210	TGTCAAGCGGTCGGATGTGCTGGAGCCCTTCGCCCGCGGTGTCAATGGAGAACTCC	269	
QY	266	AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG	325	
Ddb	270	AGCTGGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAGGCTTATTTATGCCAGGCTGAGTG	329	
QY	326	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	385	
Ddb	330	GATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT	389	
QY	386	TGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGTGAGAAATCCGTATGCCCGCTGAATC	445	
Ddb	390	TGTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGTGAGAAATCCGTATGCCCGCTGAATC	449	
QY	446	TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	505	
Ddb	450	TCCTGGCTGACTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT	509	
QY	506	TTGACCGCACACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG	565	
Ddb	510	TTGACCGCACACGCACTGACAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACAG	569	

Qy	566	CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	625
Db	570	CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG	629
Qy	626	GACAGAACATGTTGGATGGTGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	685
Db	630	GACAGAACATGTTGGATGGTGAGCACCTTCTATACGACTTACAGGACAGCAGATGGGG	689
Qy	686	AATTCTATGCTGTTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAGGACTTG	745
Db	690	AATTCTATGCTGTTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAGGACTTG	749
Qy	746	GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA	805
Db	750	GACTAAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGCCAGAAATGAAGA	809
Qy	806	AGAAGTTTCAGATGTATTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACG	865
Db	810	AGAAGTTTCAGATGTATTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACG	869
Qy	866	GCACAGATGCTGTGTGACTCCGGTCTTGACTTTTGAGGAGGTTGTTTCATCATGATCACA	925
Db	870	GCACAGATGCTGTGTGACTCCGGTCTTGACTTTTGAGGAGGTTGTTTCATCATGATCACA	929
Qy	926	ACAAGGAACGGGGCTCGTTTATCACCACTGAGGACGAGGACGTGAGCCCCCGCCCTGCAC	985
Db	930	ACAAGGAACGGGGCTCGTTTATCACCACTGAGGACGAGGACGTGAGCCCCCGCCCTGCAC	989
Qy	986	CTCTGCTGTTAAACACCCCGATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC	1045
Db	990	CTCTGCTGTTAAACACCCCGATCCCTTCTTTCAAAGGGATCCTTTTCATAGGAGAAC	1049
Qy	1046	ACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACT	1105
Db	1050	ACACTGAGGAGATACCTTGAAGAAATTTGGATTCAGCCCGGAAGAGATTTATCAGCTTAACT	1109
Qy	1106	CAGATAAAATCATTGAAAGTAATAAGGTAAAAAGCTAGTCTC	1146
Db	1110	CAGATAAAATCATTGAAAGTAATAAGGTAAAAAGCTAGTCTC	1150

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 08:12:55 ; Search time 840 Seconds
(without alignments)
8821.852 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagctagtctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0.

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1146	100.0	1146	9	US-09-967-305-3	Sequence 3, Appli
2	1146	100.0	2005	9	US-09-967-305-1	Sequence 1, Appli
3	1146	100.0	2005	9	US-09-967-305-10	Sequence 10, Appl
4	1146	100.0	2005	16	US-10-210-120-104	Sequence 104, App
5	1146	100.0	2005	22	US-10-909-035-104	Sequence 104, App
6	1146	100.0	2069	9	US-09-967-305-4	Sequence 4, Appli
7	1146	100.0	2069	15	US-10-205-823-17	Sequence 17, Appl

8	1144.4	99.9	2069	15	US-10-205-823-25	Sequence 25, Appl
9	1142.8	99.7	1621	9	US-09-759-143-107	Sequence 107, App
10	1142.8	99.7	1621	9	US-09-780-669-107	Sequence 107, App
11	1142.8	99.7	1621	9	US-09-030-606-107	Sequence 107, App
12	1142.8	99.7	1621	9	US-09-822-827-107	Sequence 107, App
13	1142.8	99.7	1621	9	US-09-115-453-107	Sequence 107, App
14	1142.8	99.7	1621	9	US-09-232-880-107	Sequence 107, App
15	1142.8	99.7	1621	9	US-09-895-793-107	Sequence 107, App
16	1142.8	99.7	1621	9	US-09-895-814-107	Sequence 107, App
17	1142.8	99.7	1621	13	US-10-012-896-107	Sequence 107, App
18	1142.8	99.7	1621	14	US-10-010-940-107	Sequence 107, App
19	1142.8	99.7	1621	16	US-10-144-678A-107	Sequence 107, App
20	1142.8	99.7	1621	16	US-10-294-025-107	Sequence 107, App
21	1142.8	99.7	1621	19	US-10-688-838-107	Sequence 107, App
22	1142.8	99.7	2376	20	US-10-357-930-21284	Sequence 21284, A
23	1142.8	99.7	2376	20	US-10-357-930-21872	Sequence 21872, A
24	1142.8	99.7	2376	20	US-10-357-930-25228	Sequence 25228, A
25	1142.8	99.7	2376	20	US-10-357-930-27126	Sequence 27126, A
26	1132	98.8	3654	9	US-09-967-305-6	Sequence 6, Appli
27	1132	98.8	3654	15	US-10-205-823-19	Sequence 19, Appl
28	1130.4	98.6	2626	15	US-10-205-823-27	Sequence 27, Appl
29	1093.4	95.4	2068	17	US-10-295-027-1134	Sequence 1134, Ap
30	1093.4	95.4	2068	19	US-10-316-540-11	Sequence 11, Appl
31	932.8	81.4	1039	17	US-10-378-029-3	Sequence 3, Appli
32	898	78.4	1294	20	US-10-357-930-22613	Sequence 22613, A
33	898	78.4	1294	20	US-10-357-930-22726	Sequence 22726, A
34	898	78.4	1294	20	US-10-357-930-27725	Sequence 27725, A
35	898	78.4	1294	20	US-10-357-930-28455	Sequence 28455, A
36	898	78.4	1294	20	US-10-357-930-28557	Sequence 28557, A
37	814	71.0	3023	9	US-09-967-305-8	Sequence 8, Appli
38	814	71.0	3023	15	US-10-205-823-21	Sequence 21, Appl
39	812.4	70.9	2946	15	US-10-205-823-29	Sequence 29, Appl
40	812.4	70.9	2946	19	US-10-316-540-13	Sequence 13, Appl
41	776.8	67.8	1504	9	US-09-917-800A-1576	Sequence 1576, Ap
42	776.8	67.8	1504	17	US-10-191-803-41	Sequence 41, Appl
43	776.8	67.8	1504	18	US-10-152-319A-1546	Sequence 1546, Ap
44	776.8	67.8	1504	21	US-10-486-706-238	Sequence 238, App
45	743.8	64.9	1316	15	US-10-205-823-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-967-305-3
; Sequence 3, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1146)
US-09-967-305-3

Query Match 100.0%; Score 1146; DB 9; Length 1146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCATCTCGGTCTGGTGGAGCTGTCGGCCTGGCCCCCGGCTTCTGT 60

Db 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGTGTCCGGCCTGGCCCCGGGCCCCGTTCTGT 60
QY 61 GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTCCCGC 120
Db 61 GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTCCCGC 120
QY 121 TACGACGTGAGCCGCTTGGGCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCCG 180
Db 121 TACGACGTGAGCCGCTTGGGCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCCG 180
QY 181 CGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240
Db 181 CGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240
QY 241 CGCCGCGGTGCATGAGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 300
Db 241 CGCCGCGGTGCATGAGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 300
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTTCGCCGTTAGCT 360
Db 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTTCGCCGTTAGCT 360
QY 361 GGCCACGATATCAACTATTGGCTTTGTAGGTTCTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 361 GGCCACGATATCAACTATTGGCTTTGTAGGTTCTCTCAAAAATTTGGCAGAAAGTGGT 420
QY 421 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGCTTATGTGT 480
Db 421 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGCTTATGTGT 480
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCAATT 540
Db 481 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCAATT 540
QY 541 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 600
Db 541 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 600
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660
Db 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660
QY 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTT 720
Db 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTT 720
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGATGAGC 780
Db 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAATTCCTCAATCAGATGAGC 780
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAGAAAGACGAAG 840
Db 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAGAAAGACGAAG 840
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 900
Db 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTTCTGACTTTT 900
QY 901 GAGGAGTGTGTTTCATCATGATCACAACAGGAACGGGCTCGTTTATCACCAAGTGGAG 960
Db 901 GAGGAGTGTGTTTCATCATGATCACAACAGGAACGGGCTCGTTTATCACCAAGTGGAG 960
QY 961 CAGGAGTGGCCCCCGCTTCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 961 CAGGAGTGGCCCCCGCTTCACCTCTGCTGTTTAAACACCCAGCCATCCCTTCTTTC 1020
QY 1021 AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTGAGC 1080
Db 1021 AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAAATTTGGATTGAGC 1080
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATTGAAAGTAATAAGGTAAAAGCT 1140

Db 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAAGCT 1140
QY 1141 AGTCTC 1146
Db 1141 AGTCTC 1146
RESULT 2
US-09-967-305-1
; Sequence 1, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-305-1

Query Match 100.0%; Score 1146; DB 9; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGTGTCCGGCCTGGCCCCGGGCCCCGTTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGTGTCCGGCCTGGCCCCGGGCCCCGTTCTGT 125
QY 61 GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTCCCGC 120
Db 126 GCTATGGTCTTGCTGACTTTCGGGGCGCGTGTGGTACGCGTGGACCGGCGCGCTCCCGC 185
QY 121 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCCG 180
Db 186 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTCTGGACCTGAAGCAGCCG 245
QY 181 CGGGAGCCGCGTGTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240
Db 246 CGGGAGCCGCGTGTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 305
QY 241 CGCCGCGGTGCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 300
Db 306 CGCCGCGGTGCATGGAGAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAGAAATCCA 365
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTTCGCCGTTAGCT 360
Db 366 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCCAGGAAGCTTTCGCCGTTAGCT 425
QY 361 GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 426 GGCCACGATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGGT 485
QY 421 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGCGCTTATGTGT 480
Db 486 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGTGGTGGCGCTTATGTGT 545
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCAATT 540
Db 546 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCAATT 605
QY 541 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 600
Db 606 GATGCAAAATATGGTGAAGGAAACAGCATATTTAAAGTCTTTTCTGTGGAAAACTCAGAAA 665

QY 601 TCGAGTCTGTGGGAAGCAGCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660
Db 666 TCGAGTCTGTGGGAAGCAGCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 725
QY 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 726 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAGAACGGAAG 840
Db 846 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAGAACGGAAG 905
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGACTCCGGTTCGACTTTT 900
Db 906 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGACTCCGGTTCGACTTTT 965
QY 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCACTGAGGAG 960
Db 966 GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCACTGAGGAG 1025
QY 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGGATCCTTTCTAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1080
Db 1086 AAAAGGGATCCTTTCTAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1145
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAAGCT 1140
Db 1146 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 3
US-09-967-305-10
; Sequence 10, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

Query Match 100.0%; Score 1146; DB 9; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCGGCCCTGGCCCGGCGGCTTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCGGCCCTGGCCCGGCGGCTTCTGT 125

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGGCTCCCGC 120
Db 126 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGGCTCCCGC 185
QY 121 TACGACGTAGCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db 186 TACGACGTAGCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 245
QY 181 CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGCGAGCCCTTC 240
Db 246 CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTGCGATGTGCTGCGAGCCCTTC 305
QY 241 CGCCCGCGTGTCAATGGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db 306 CGCCCGCGTGTCAATGGAGAAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 365
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTAGCT 360
Db 366 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTAGCT 425
QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 420
Db 426 GGCCACGATATCAACTATTTGGCTTTGTCAAGTGTCTCTCAAAAATTTGGCAGAAAGTGT 485
QY 421 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 486 GAGAAATCCGTATGCCCGCTGAATCTCTGCTGCTGACTTTGCTGGTGGCTTATGTGT 545
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGCTCAGGTCAAT 540
Db 546 GCACTGGGCATTATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGCTCAGGTCAAT 605
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 600
Db 606 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 665
QY 601 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 660
Db 666 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTCTAT 725
QY 661 ACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 726 ACGACTTACAGGACAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAGAACGGAAG 840
Db 846 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCCAAGAACGGAAG 905
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT 900
Db 906 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCGACTTTT 965
QY 901 GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCACTGAGGAG 960
Db 966 GAGGAGTGTTCATCATGATCAACAAGGAACGGGCTCGTTTATCACCACTGAGGAG 1025
QY 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGGATCCTTTCTAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1080
Db 1086 AAAAGGGATCCTTTCTAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC 1145
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAAGCT 1140
Db 1146 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAAAGCT 1205

```
QY      1141 AGTCTC 1146
Db      1206 AGTCTC 1211

RESULT 4
US-10-210-120-104
; Sequence 104, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-104

Query Match      100.0%; Score 1146; DB 16; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGCCGGCCCTGGCCCCCGGCGTTCGT 60
Db      |||||||
66 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGCCGGCCCTGGCCCCCGGCGTTCGT 125

QY      61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGCCGCTCCCGC 120
Db      |||||||
126 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGGCCGCTCCCGC 185

QY      121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db      |||||||
186 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 245

QY      181 CGGGAGCGCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGCGAGCCCTTC 240
Db      |||||||
246 CGGGAGCGCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGCGAGCCCTTC 305

QY      241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAAATCCA 300
Db      |||||||
306 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAAATCCA 365

QY      301 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db      |||||||
366 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425

QY      361 GGCCACGATATCAACTATTGGCTTTGTACGGTGTCTCTCAAAAATTGGCAGAAAGTGGT 420
Db      |||||||
426 GGCCACGATATCAACTATTGGCTTTGTACGGTGTCTCTCAAAAATTGGCAGAAAGTGGT 485

QY      421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db      |||||||
486 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 545

QY      481 GCACTGGGCATTATAATGGTCTTTTGTACCGCACACGCACTGGCAAGGGTCAGGTCATT 540
Db      |||||||
546 GCACTGGGCATTATAATGGTCTTTTGTACCGCACACGCACTGGCAAGGGTCAGGTCATT 605

QY      541 GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTCTGTGGAAACTCAGAAA 600
Db      |||||||
606 GATGCAAAATATGGTGGAGGAACAGCATATTTAAAGTTCTTTTCTGTGGAAACTCAGAAA 665
```

```
QY      601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db      |||||||
666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 725

QY      661 ACGACTTACAGGACAGCAGATGGGAATTCTATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db      |||||||
726 ACGACTTACAGGACAGCAGATGGGAATTCTATGGCTGTTGGAGCAATAGAACCCAGTTC 785

QY      721 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db      |||||||
786 TACGAGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845

QY      781 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTGCAAAAGAACGAAG 840
Db      |||||||
846 ATGGATGATTGGCCAGAAATGAAGAAAGTTTGCAGATGTATTTGCAAAAGAACGAAG 905

QY      841 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCGACTTTT 900
Db      |||||||
906 GCAGAGTGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCGACTTTT 965

QY      901 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 960
Db      |||||||
966 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 1025

QY      961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCATCCCTTCTTTC 1020
Db      |||||||
1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCATCCCTTCTTTC 1085

QY      1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGTAATTGGATT 1080
Db      |||||||
1086 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGTAATTGGATT 1145

QY      1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAATAAGGTAAGCT 1140
Db      |||||||
1146 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAATAAGGTAAGCT 1205

QY      1141 AGTCTC 1146
Db      |||||||
1206 AGTCTC 1211

RESULT 5
US-10-909-035-104
; Sequence 104, Application US/10909035
; Publication No. US20050136493A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Mark A.
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Laxman, Bharathi
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: AMACR Cancer Markers
; FILE REFERENCE: UM-09098
; CURRENT APPLICATION NUMBER: US/10/909,035
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-909-035-104

Query Match      100.0%; Score 1146; DB 22; Length 2005;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGCACTGCAGGCATCTCGGTCTGTGGAGCTGCCGGCCTGGCCCCCGGCGTTCGT 60
Db      |||||||
66 ATGGCACTGCAGGCATCTCGGTCTGTGGAGCTGCCGGCCTGGCCCCCGGCGTTCGT 125

QY      61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTCCCGC 120
Db      |||||||
126 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCGCTCCCGC 185
```

QY	121	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG	180
Db	186	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG	245
QY	181	CGGGAGCCGCGTGTCTGCGGCTCTGTGCAAGCGTCCGATGTCTGCTGGAGCCCTTC	240
Db	246	CGGGAGCCGCGTGTCTGCGGCTCTGTGCAAGCGTCCGATGTCTGCTGGAGCCCTTC	305
QY	241	CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA	300
Db	306	CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA	365
QY	301	AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT	360
Db	366	AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT	425
QY	361	GGCCACGATATCAACTATTTGGCTTTGTCAAGGTCTCTCAAAAAATGGCAGAAAGTGT	420
Db	426	GGCCACGATATCAACTATTTGGCTTTGTCAAGGTCTCTCAAAAAATGGCAGAAAGTGT	485
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGGTGGTGGCTTATGTGT	480
Db	486	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTTGGTGGTGGCTTATGTGT	545
QY	481	GCACCTGGGCATTATATGGCTCTTTTTCACCGCACACGCACTGGCAAGGTCAGGTCAAT	540
Db	546	GCACCTGGGCATTATATGGCTCTTTTTCACCGCACACGCACTGGCAAGGTCAGGTCAAT	605
QY	541	GATGCAAAATATGGTGGAAAGCACTCGAGGACAGCAATATTTAAGTTCTTTTCTGAGCACTTCTAT	600
Db	606	GATGCAAAATATGGTGGAAAGCACTCGAGGACAGCAATATTTAAGTTCTTTTCTGAGCACTTCTAT	665
QY	601	TCGAGTCTGTGGAAAGCACTCGAGGACAGCAATATTTAAGTTCTTTTCTGAGCACTTCTAT	660
Db	666	TCGAGTCTGTGGAAAGCACTCGAGGACAGCAATATTTAAGTTCTTTTCTGAGCACTTCTAT	725
QY	661	ACGACTTACAGGACAGCAGATGGGAAATTCTATGGCTGTGTGGAGCAATAGAACCCCAAGTTC	720
Db	726	ACGACTTACAGGACAGCAGATGGGAAATTCTATGGCTGTGTGGAGCAATAGAACCCCAAGTTC	785
QY	721	TACGAGCTGTGATCAAAGCACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC	780
Db	786	TACGAGCTGTGATCAAAGCACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC	845
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAAGAGACGAAG	840
Db	846	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAAGAGACGAAG	905
QY	841	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	900
Db	906	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT	965
QY	901	GAGGAGGTTGTTTCATCATGTATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	960
Db	966	GAGGAGGTTGTTTCATCATGTATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	1025
QY	961	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1020
Db	1026	CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1085
QY	1021	AAAAGGGATCCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1080
Db	1086	AAAAGGGATCCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1145
QY	1081	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT	1140
Db	1146	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT	1205
QY	1141	AGTCTC	1146
Db	1206	AGTCTC	1211

```

RESULT 6
US-09-967-305-4
; Sequence 4, Application US/09967305
; Patent No. US20020123081A1
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALP
; TITLE OF INVENTION: REFRACTORY AND METAS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(1235)
US-09-967-305-4

```

	Query Match	100.0%;	Score 1146;	DB 9;	Length 2069;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1146;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCACTGACGGGCATCTCGTCTGTGGAGCTGTCCGGCCCTGGCCCGGGCCCGCTTCTGT	60		
DB	90	ATGGCACTGACGGGCATCTCGTCTGTGGAGCTGTCCGGCCCTGGCCCGGGCCCGCTTCTGT	149		
QY	61	GCTATGGTCTTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC	120		
DB	150	GCTATGGTCTTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC	209		
QY	121	TACGACGTAGCCGCTTGGGCCCGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG	180		
DB	210	TACGACGTAGCCGCTTGGGCCCGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG	269		
QY	181	CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC	240		
DB	270	CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC	329		
QY	241	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGCAGCGGGAAATCCA	300		
DB	330	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCCGAGAGATTCTGCAGCGGGAAATCCA	389		
QY	301	AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360		
DB	390	AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	449		
QY	361	GGCCACGATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATGGCAGAAGTGT	420		
DB	450	GGCCACGATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATGGCAGAAGTGT	509		
QY	421	GAGAACTCGATGCCCGCTGAATCTCCTGGCTGACTTTGCTGCTGGCTTATGTGT	480		
DB	510	GAGAACTCGATGCCCGCTGAATCTCCTGGCTGACTTTGCTGCTGGCTTATGTGT	569		
QY	481	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAAT	540		
DB	570	GCACTGGGCATTATAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAAT	629		
QY	541	GATGCAATAATGGTGGAAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA	600		
DB	630	GATGCAATAATGGTGGAAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAAACTCAGAAA	689		
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	660		
DB	690	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT	749		


```
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 809

QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGTGATGAACCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGTGATGAACCTCCCAATCAGATGAGC 869

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAACGGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAACGGAAG 929

QY 841 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 900
Db 930 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 989

QY 901 GAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 960
Db 990 GAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 1049

QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1109

QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1080
Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1169

QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTAAAAGCT 1140
Db 1170 CGCGAAGAGATTTATCAGCTTAACCTCAGATAAAATCATTGAAAGTAATAAGGTAAAAGCT 1229

QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235
```

```
RESULT 7
US-10-205-823-17
; Sequence 17, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
```

```
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-17

Query Match      100.0%; Score 1146; DB 15; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGTGGAGCTGTCCGGCCTGGCCCGGGCCCGTTCGT 60
Db 90 ATGGCACTGCAGGGCATCTCGTCTGTGGAGCTGTCCGGCCTGGCCCGGGCCCGTTCGT 149

QY 61 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 120
Db 150 GCTATGCTCTGGCTGACTTCGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 209

QY 121 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 269

QY 181 CGGGAGCCCGCTGTCTCGGCGTCTGTGCAAGCGGTGGATGTCTGTGGAGCCCTTC 240
Db 270 CGGGAGCCCGCTGTCTCGGCGTCTGTGCAAGCGGTGGATGTCTGTGGAGCCCTTC 329

QY 241 CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCGCAGAGATTCTGACGGGGAATAATCCA 300
Db 330 CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCGCAGAGATTCTGACGGGGAATAATCCA 389

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGTCTCTCAAAAATGGCAGAAGTGGT 420
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGTCTCTCAAAAATGGCAGAAGTGGT 509

QY 361 GGCCACGATATCAACTATTTGGCTTTGTCTAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 420
Db 450 GGCCACGATATCAACTATTTGGCTTTGTCTAGGTGTTCTCTCAAAAATGGCAGAAGTGGT 509

QY 421 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 480
Db 510 GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT 569

QY 481 GCACCTGGGCATTAATGGCTCTTTTGGACCGCACACGACTGGCAAGGTCAGGTCAAT 540
Db 570 GCACCTGGGCATTAATGGCTCTTTTGGACCGCACACGACTGGCAAGGTCAGGTCAAT 629

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTAAGTCTTTTCTGTGGAATACTCAGAAA 600
Db 630 GATGCAAAATATGGTGAAGGAACAGCATATTAAGTCTTTTCTGTGGAATACTCAGAAA 689

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACTTTCTAT 660
Db 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACTTTCTAT 749

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 809

QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 869

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAACGGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTCAGATGTATTTGCAAAAGAACGGAAG 929

QY 841 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 900
Db 930 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCGACTTTT 989

QY 901 GAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 960
Db 990 GAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAAGTGAGGAG 1049
```


QY 961 CAGGAGTGGCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1020
| | | | |
Db 1050 CAGGAGTGGCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1109
| | | | |
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
| | | | |
Db 1110 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1169
| | | | |
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT 1140
| | | | |
Db 1170 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT 1229
| | | | |
QY 1141 AGTCTC 1146
| | | | |
Db 1230 AGTCTC 1235
| | | | |

RESULT 8
US-10-205-823-25
; Sequence 25, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkár, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-25

Query Match 99.9%; Score 1144.4; DB 15; Length 2069;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCGT 60
| | | | |
Db 90 ATGGCACTGCAGGGCATCTCGGTGCTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCGT 149
| | | | |
QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGGTGGACCGGCCCGCTCCCGC 120
| | | | |
Db 150 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGGTGGACCGGCCCGCTCCCGC 209
| | | | |
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
| | | | |
Db 210 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 269
| | | | |

QY 181 CGGGAGCCCGCGTGTGCGGCGTCTGTGCAAGCGTCGGATGTGCTGCTGGAGCCCTTC 240
| | | | |
Db 270 CGGGAGCCCGCGTGTGCGGCGTCTGTGCAAGCGTCGGATGTGCTGCTGGAGCCCTTC 329
| | | | |
QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGGAAAAATCCA 300
| | | | |
Db 330 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGGAAAAATCCA 389
| | | | |
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 360
| | | | |
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 449
| | | | |
QY 361 GGCCACGATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTTGGCAGAGTGGT 420
| | | | |
Db 450 GGCCACGATATCAACTATTTGGCTTTGTCAAGGTGTCTCTCAAAAATTTGGCAGAGTGGT 509
| | | | |
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480
| | | | |
Db 510 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 569
| | | | |
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGTCAGGTCAATT 540
| | | | |
Db 570 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGACAAGGTCAGGTCAATT 629
| | | | |
QY 541 GATGCAAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 600
| | | | |
Db 630 GATGCAAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAATACTCAGAAA 689
| | | | |
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 660
| | | | |
Db 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 749
| | | | |
QY 661 ACGACTTACAGGCACAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720
| | | | |
Db 750 ACGACTTACAGGCACAGATGGGAAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 809
| | | | |
QY 721 TACGAGTCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 780
| | | | |
Db 810 TACGAGTCTGTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC 869
| | | | |
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACATGATGATTTTGCAGATGATTTGCAAGCAG 840
| | | | |
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGATTTGACATGATGATTTTGCAGATGATTTGCAAGCAG 929
| | | | |
QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGTTCTGACTTTT 900
| | | | |
Db 930 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGTTCTGACTTTT 989
| | | | |
QY 901 GAGGAGTGTGTTTCATCATGATCACAACAAAGGAGCGGGCTCGTTTATCACCAGTGAGGAG 960
| | | | |
Db 990 GAGGAGTGTGTTTCATCATGATCACAACAAAGGAGCGGGCTCGTTTATCACCAGTGAGGAG 1049
| | | | |
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1020
| | | | |
Db 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1109
| | | | |
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
| | | | |
Db 1110 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1169
| | | | |
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT 1140
| | | | |
Db 1170 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGGCT 1229
| | | | |
QY 1141 AGTCTC 1146
| | | | |
Db 1230 AGTCTC 1235
| | | | |

RESULT 9
US-09-759-143-107
; Sequence 107, Application US/09759143
; Patent No. US20020022248A1

```
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-107

Query Match      99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGGCCCGTTCTGT 60
Db      5  ATGGCACTGCAGGGCATCTCGGTCTATGGAGCTGTCCGGCCTGGCCCCGGGCCCGTTCTGT 64

QY      61  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGFPACGCGTGGACCGGCCCGCTCCCGC 120
Db      65  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTGTACGCGTGGACCGGCCCGCTCCCGC 124

QY      121  TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG 180
Db      125  TACGACGTGAGCCGCTTGGCCCGGGGCAAGCGCTCGCTAGTGTCTGGACCTGAAGCAGCCG 184

QY      181  CGGGGAGCCCGCGTGTCTGGCGCGTCTGTGCAAGCGGTCGGATGTGCTGTGGAGCCCTTC 240
Db      185  CGGGGAGCCCGCGTGTCTGGCGCGTCTGTGCAAGCGGTCGGATGTGCTGTGGAGCCCTTC 244

QY      241  CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAATAATCCA 300
Db      245  CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGGAATAATCCA 304

QY      301  AGSCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db      305  AGSCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364

QY      361  GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 420
Db      365  GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAAGTGT 424

QY      421  GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 480
Db      425  GAGAAATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 484

QY      481  GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGGCAAGGGTCAGTCAAT 540
Db      485  GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCACTGCAAGGGTCAGTCAAT 544

QY      541  GATGCAATATGGTGGAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
```

```
Db      545  GATGCAAAATATGGTGGAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA 604
QY      601  TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db      605  TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTTCTAT 664
QY      661  ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db      665  ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
QY      721  TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db      725  TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY      781  ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAAGAACGAAG 840
Db      785  ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAAAGAACGAAG 844
QY      841  GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGACTTTT 900
Db      845  GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGACTCCGGTTCTGACTTTT 904
QY      901  GAGGAGTGTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 960
Db      905  GAGGAGTGTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAAGTGAAG 964
QY      961  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCCAGCCATCCCTTCTTTC 1020
Db      965  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCCCAGCCATCCCTTCTTTC 1024
QY      1021  AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTGGATTTCAGC 1080
Db      1025  AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTGGATTTCAGC 1084
QY      1081  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTGAAAAGTAATAAGGTAAAAGCT 1140
Db      1085  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTGAAAAGTAATAAGGTAAAAGCT 1144
QY      1141  AGTCTC 1146
Db      1145  AGTCTC 1150

RESULT 10
US-09-780-669-107
; Sequence 107, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
```

```

; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-107

Query Match          99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCCGGGCCCGGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCCGGGCCCGGTTCTGT 64

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCCCGCTCCGC 120
Db 65 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCCCGCTCCGC 124

QY 121 TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGGCGCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCCCTTC 240
Db 185 CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGTGGAGCCCTTC 244

QY 241 CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db 245 CGCGCGGTGTGATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 304

QY 301 AGGCTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTAGCT 360
Db 305 AGGCTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTAGCT 364

QY 361 GGCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420
Db 365 GGCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 424

QY 421 GACAATCCGTATGCCCCCGTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT 480
Db 425 GAGAATCCGTATGCCCCCGTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT 484

QY 481 GCACTGGGCATTATAATGGCTCTTTTGTACCGCACACGACTGGCAAGGTGAGTCAAT 540
Db 485 GCACTGGGCATTATAATGGCTCTTTTGTACCGCACACGACTGGCAAGGTGAGTCAAT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTAAAGTTCTTTCTGTGAAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTAAAGTTCTTTCTGTGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGGAATTTCATGGCTGTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTGCAAGAAGACGGAAG 840
Db 785 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTGCAAGAAGACGGAAG 844

QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 904

QY 901 GAGGAGGTTGTTTCATCATGATCAACAAGAAACGGGGCTCGTTTATCACCAGTGAGGAG 960
```

```

|||||
Db 905 GAGGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
|||||
QY 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
|||||
Db 965 CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1024
|||||
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
|||||
Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1084
|||||
QY 1081 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGAGCT 1140
|||||
Db 1085 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGGTAAGAGCT 1144
|||||
QY 1141 AGTCTC 1146
|||||
Db 1145 AGTCTC 1150
|||||

RESULT 11
US-09-030-606-107
; Sequence 107, Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-107

Query Match          99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCCGGGCCCGGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCTGGCCCCGGGCCCGGTTCTGT 64

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGGTACGGTGGACCGGCCCGCTCCGC 120
```

Db 65 GCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180

Db 125 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 184

QY 181 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240

Db 185 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 244

QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGGAAAAATCCA 300

Db 245 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGGAAAAATCCA 304

QY 301 AGGCTTATTTATGCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360

Db 305 AGGCTTATTTATGCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364

QY 361 GGCCACGATATCAACTATTTGGCTTTGTACGCTGTTCTCTCAAAAAATTGGCAGAAAGTGGT 420

Db 365 GGCCACGATATCAACTATTTGGCTTTGTACGCTGTTCTCTCAAAAAATTGGCAGAAAGTGGT 424

QY 421 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 480

Db 425 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 484

QY 481 GCACTGGGCATTAATAATGGCTCTTTTGTACCGCACAGCACTGGCAAGGTCAGGTCATT 540

Db 485 GCACTGGGCATTAATAATGGCTCTTTTGTACCGCACAGCACTGACAAGGTCAGGTCATT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGATTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGATTC 724

QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780

Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGGAAG 840

Db 785 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGGAAG 844

QY 841 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 900

Db 845 GCAGAGTGGTGCAAAATCTTTGACGGCACAGATGCTGTGACTCCGGTTCTGACTTTT 904

QY 901 GAGGAGGTTGTTCAATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960

Db 905 GAGGAGGTTGTTCAATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964

QY 961 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020

Db 965 CAGGACGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024

QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATPACTTGAAGAAATTTGGATTGAGC 1080

Db 1025 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATPACTTGAAGAAATTTGGATTGAGC 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGAGCT 1140

Db 1085 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGAGCT 1144

QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

RESULT 12

US-09-822-827-107

; Sequence 107, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; CURRENT FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-822-827-107

Query Match 99.7%; Score 1142.8; DB 9; Length 1621;

Best Local Similarity 99.8%; Pred.No. 0;

Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCTGGCCCGGGCCCGTTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCCGGCTGGCCCGGGCCCGTTCTGT 64

QY 61 GCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 120

Db 65 GCTATGCTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG 180

Db 125 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGTAGTGTGGAACCTGAAGCAGCCG 184

QY 181 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240

Db 185 CGGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 244

QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGGAAAAATCCA 300

Db 245 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCCAGAGATTCCTGACGGGGGAAAAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360

Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 364

QY 361 GGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGSCAGAAAGTGGT 420

Db 365 GGCCACGATATCAACTATTTGGCTTTGTACAGTGTCTCTCAAAAAATTGSCAGAAAGTGGT 424

QY 421 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 480

Db 425 GAGAAATCCGATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGT 484

QY 481 GCACTGGGCATTAATAATGGCTCTTTTGTACCGCACAGCACTGGCAAGGTCAGGTCATT 540

Db 485 GCACTGGGCATTAATAATGGCTCTTTTGTACCGCACAGCACTGACAAGGTCAGGTCATT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAA 600

Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCAT 660

Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGATTC 720

Db 665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCGATTC 724

QY	721	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	780
Db	725	TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTTCCCAATCAGATGAGC	784
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGGAAG	840
Db	785	ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAGACGGAAG	844
QY	841	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTGACTTTT	900
Db	845	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTCTGACTTTT	904
QY	901	GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	960
Db	905	GAGGAGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG	964
QY	961	CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC	1020
Db	965	CAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC	1024
QY	1021	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1080
Db	1025	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1084
QY	1081	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTGAAAAGTAATAAGGTAAAAGCT	1140
Db	1085	CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTGAAAAGTAATAAGGTAAAAGCT	1144
QY	1141	AGTCTC 1146	
Db	1145	AGTCTC 1150	
RESULT 13			
US-09-115-453-107			
; Sequence 107, Application US/09115453B			
; Patent No. US20020090372A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND			
; TITLE OF INVENTION: METHODS FOR THEIR USE			
; FILE REFERENCE: 210121.427C4			
; CURRENT APPLICATION NUMBER: US/09/115,453B			
; CURRENT FILING DATE: 1998-07-14			
; NUMBER OF SEQ ID NOS: 228			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 107			
; LENGTH: 1621			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-115-453-107			

QY	241	CGCCGCGGTGTCATGAGAAACTCCAGCTGGGCCACAGATTCTGCAGCGGGAATAATCCA	300
Db	245	CGCCGCGGTGTCATGAGAAACTCCAGCTGGGCCACAGATTCTGCAGCGGGAATAATCCA	304
QY	301	AGGCTTATTTATGCCAGGCTGAGTGGATTGCGCCAGTCAGGAAGCTTCTGCGGTTAGCT	360
Db	305	AGGCTTATTTATGCCAGGCTGAGTGGATTGCGCCAGTCAGGAAGCTTCTGCGGTTAGCT	364
QY	361	GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAAATTGGCAGAAAGTGGT	420
Db	365	GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAAATTGGCAGAAAGTGGT	424
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT	480
Db	425	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGT	484
QY	481	GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACCTGGCAAGGTCAGSTCATT	540
Db	485	GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACACGCACCTGGCAAGGTCAGSTCATT	544
QY	541	GATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	600
Db	545	GATGCAAAATATGTTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCAGAAA	604
QY	601	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT	660
Db	605	TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT	664
QY	661	ACGACTTACAGGACAGCAGATGGGGAATTCATGSGCTGTTGGAGCAATAGAACCCAGTTTC	720
Db	665	ACGACTTACAGGACAGCAGATGGGGAATTCATGSGCTGTTGGAGCAATAGAACCCAGTTTC	724
QY	721	TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC	780
Db	725	TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC	784
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGCAAAAGAACGAAAG	840
Db	785	ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGCAAAAGAACGAAAG	844
QY	841	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGACTTTT	900
Db	845	GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTTGACTTTT	904
QY	901	GAGGAGGTTGTTTCATCATGATCACAAACAAGGAACGGGGCTCGTTTATCACCACTGAGGAG	960
Db	905	GAGGAGGTTGTTTCATCATGATCACAAACAAGGAACGGGGCTCGTTTATCACCACTGAGGAG	964
QY	961	CAGGACGTGAGCCCCCGCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1020
Db	965	CAGGACGTGAGCCCCCGCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTC	1024
QY	1021	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1080
Db	1025	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTGAGC	1084
QY	1081	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAAATCATTTGAAAGTAATAAGGTAAAAGCT	1140
Db	1085	CGCGAAGAGATTTATCAGCTTAACTCAGATAAAAATCATTTGAAAGTAATAAGGTAAAAGCT	1144
QY	1141	AGTCTC	1146
Db	1145	AGTCTC	1150

RESULT 14
US-09-232-880-107
; Sequence 107, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn

```

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-107

Query Match          99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTATGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCTGT 64

QY 61 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAGACCGGCGGCTCCCGC 120
Db 65 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAGACCGGCGGCTCCCGC 124

QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
Db 125 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 184

QY 181 CGGGAGCCGCGCTGCTCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 240
Db 185 CGGGAGCCGCGCTGCTCGCGCGTCTGTGCAAGCGGTGCGATGTGCTGTGAGCCCTTC 244

QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCGCAGAGATTCTGCAGCGGGAAATCCA 300
Db 245 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCGCAGAGATTCTGCAGCGGGAAATCCA 304

QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCCGGTTAGCT 360
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTTCGCCGGTTAGCT 364

QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAAATTCGAGAAAGTGGT 420
Db 365 GGCCACGATATCAACTATTGGCTTTGTGAGGTCTCTCAAAAATTCGAGAAAGTGGT 424

QY 421 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 425 GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 484

QY 481 GCACCTGGCATTATATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCAAT 540
Db 485 GCACCTGGCATTATATGGCTCTTTTGGACCGCACAGCACTGACAAAGGTCAGGTCAAT 544

QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTCTTTTCTGTGGAAACTCAGAAA 604

QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db 605 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 664

QY 661 ACGACTTACAGGACAGCAGATGGGGAATTATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACGACTTACAGGACAGCAGATGGGGAATTATGGCTGTTGGAGCAATAGAACCCAGTTC 724

QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 784

QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGGAGATGTATTTGCAAGAAGACGAAG 840
Db 785 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGGAGATGTATTTGCAAGAAGACGAAG 844
```

```

QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904

QY 901 GAGGAGTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964

QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db 965 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1024

QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1080
Db 1025 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTGAGC 1084

QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAAATCATTGAAAAGTAATAAGGTAAAAGCT 1140
Db 1085 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAAATCATTGAAAAGTAATAAGGTAAAAGCT 1144

QY 1141 AGTCTC 1146
Db 1145 AGTCTC 1150

RESULT 15
US-09-895-793-107
; Sequence 107, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-107
```

```

Query Match          99.7%; Score 1142.8; DB 9; Length 1621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCTGT 60
Db 5 ATGGCACTGCAGGGCATCTCGGTCTATGGAGCTGTCCGGCCTGGCCCCGGCCCGTTCTGT 64
```

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAGCCGCGCCCGCTCCCGC 120
Db ||||| 1145 AGTCTC 1150
65 GCTATGGTCTTGGCTGACTTCGGGGCGCGTGTGTACGCGTGAGCCGCGCCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG 180
Db ||||| 1145 AGTCTC 1150
125 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGTAGTGTCTGGACCTGAAGCAGCCG 184
QY 181 CGGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 240
Db ||||| 1145 AGTCTC 1150
185 CGGGGAGCCGCGTCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGTGAGCCCTTC 244
QY 241 CGCCGCGGTGTATGAGAGAACTCCAGCTGGGCCCAGAGATTCTGACGGGAAATCCA 300
Db ||||| 1145 AGTCTC 1150
245 CGCCGCGGTGTATGAGAGAACTCCAGCTGGGCCCAGAGATTCTGACGGGAAATCCA 304
QY 301 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db ||||| 1145 AGTCTC 1150
305 AGGCTTATTTATGCCAGGTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 364
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db ||||| 1145 AGTCTC 1150
365 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAAGTGT 424
QY 421 GAGAAATCCGTATGCCCGCGTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480
Db ||||| 1145 AGTCTC 1150
425 GAGAAATCCGTATGCCCGCGTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 484
QY 481 GCACCTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGGTCAGGTCATT 540
Db ||||| 1145 AGTCTC 1150
485 GCACCTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGGTCAGGTCATT 544
QY 541 GATGCAAAATANGTGAAGGAACAGCATAATTTAAGTTCTTTCTGTGGAATACTCAGAAA 600
Db ||||| 1145 AGTCTC 1150
545 GATGCAAAATANGTGAAGGAACAGCATAATTTAAGTTCTTTCTGTGGAATACTCAGAAA 604
QY 601 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 660
Db ||||| 1145 AGTCTC 1150
605 TCGAGTCTGTGGGAAGCACTTCGAGGACAGAACATGTTGGATGGTGGAGCACTTTCTAT 664
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db ||||| 1145 AGTCTC 1150
665 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db ||||| 1145 AGTCTC 1150
725 TACGAGCTGTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAGAAGACGAAG 840
Db ||||| 1145 AGTCTC 1150
785 ATGGATGATTGGCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAGAAGACGAAG 844
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db ||||| 1145 AGTCTC 1150
845 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db ||||| 1145 AGTCTC 1150
905 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTTC 1020
Db ||||| 1145 AGTCTC 1150
965 CAGGACGTGAGCCCCCGCCTGCACCTCTGTGTTAAACACCCAGCCATCCCTTCTTTTC 1024
QY 1021 AAAAGGGATCCCTTTCATAGGAGAACACACTGAGGAGATACTTTGAAGAATTTGGATTGAGC 1080
Db ||||| 1145 AGTCTC 1150
1025 AAAAGGGATCCCTTTCATAGGAGAACACACTGAGGAGATACTTTGAAGAATTTGGATTGAGC 1084
QY 1081 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGAGCT 1140
Db ||||| 1145 AGTCTC 1150
1085 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGAGCT 1144
QY 1141 AGTCTC 1146

Db ||||| 1145 AGTCTC 1150

Search completed: July 27, 2005, 10:55:51
Job time : 844 secs

THIS PAGE IS BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 06:57:54 ; Search time 5000 Seconds
(without alignments)
9356.642 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagctagtctc 1146

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA Main:
1: /cgn2_6/ptodata/1/pna/PCTUS1 COMB.seq:
2: /cgn2_6/ptodata/1/pna/PCTUS2 COMB.seq:
3: /cgn2_6/ptodata/1/pna/PCTUS COMB.seq:
4: /cgn2_6/ptodata/1/pna/US06 COMB.seq:
5: /cgn2_6/ptodata/1/pna/US07 COMB.seq:
6: /cgn2_6/ptodata/1/pna/US080 COMB.seq:
7: /cgn2_6/ptodata/1/pna/US081 COMB.seq:
8: /cgn2_6/ptodata/1/pna/US082 COMB.seq:
9: /cgn2_6/ptodata/1/pna/US083 COMB.seq:
10: /cgn2_6/ptodata/1/pna/US084 COMB.seq:
11: /cgn2_6/ptodata/1/pna/US085 COMB.seq:
12: /cgn2_6/ptodata/1/pna/US086 COMB.seq:
13: /cgn2_6/ptodata/1/pna/US087 COMB.seq:
14: /cgn2_6/ptodata/1/pna/US088 COMB.seq:
15: /cgn2_6/ptodata/1/pna/US089 COMB.seq:
16: /cgn2_6/ptodata/1/pna/US090 COMB.seq:
17: /cgn2_6/ptodata/1/pna/US091 COMB.seq:
18: /cgn2_6/ptodata/1/pna/US092A COMB.seq:
19: /cgn2_6/ptodata/1/pna/US092B COMB.seq:
20: /cgn2_6/ptodata/1/pna/US093A COMB.seq:
21: /cgn2_6/ptodata/1/pna/US093B COMB.seq:
22: /cgn2_6/ptodata/1/pna/US094 COMB.seq:
23: /cgn2_6/ptodata/1/pna/US095A COMB.seq:
24: /cgn2_6/ptodata/1/pna/US095B COMB.seq:
25: /cgn2_6/ptodata/1/pna/US095C COMB.seq:
26: /cgn2_6/ptodata/1/pna/US095D COMB.seq:
27: /cgn2_6/ptodata/1/pna/US096A COMB.seq:
28: /cgn2_6/ptodata/1/pna/US096B COMB.seq:
29: /cgn2_6/ptodata/1/pna/US096C COMB.seq:
30: /cgn2_6/ptodata/1/pna/US096D COMB.seq:
31: /cgn2_6/ptodata/1/pna/US096E COMB.seq:
32: /cgn2_6/ptodata/1/pna/US097A COMB.seq:
33: /cgn2_6/ptodata/1/pna/US097B COMB.seq:
34: /cgn2_6/ptodata/1/pna/US097C COMB.seq:
35: /cgn2_6/ptodata/1/pna/US098A COMB.seq:
36: /cgn2_6/ptodata/1/pna/US098B COMB.seq:
37: /cgn2_6/ptodata/1/pna/US098C COMB.seq:
38: /cgn2_6/ptodata/1/pna/US098D COMB.seq:
39: /cgn2_6/ptodata/1/pna/US099A COMB.seq:
40: /cgn2_6/ptodata/1/pna/US099B COMB.seq:
41: /cgn2_6/ptodata/1/pna/US099C COMB.seq:
42: /cgn2_6/ptodata/1/pna/US099D COMB.seq:
43: /cgn2_6/ptodata/1/pna/US099E COMB.seq:

44: /cgn2_6/ptodata/1/pna/US099F COMB.seq:
45: /cgn2_6/ptodata/1/pna/US099G COMB.seq:
46: /cgn2_6/ptodata/1/pna/US100A COMB.seq:
47: /cgn2_6/ptodata/1/pna/US100B COMB.seq:
48: /cgn2_6/ptodata/1/pna/US101A COMB.seq:
49: /cgn2_6/ptodata/1/pna/US101B COMB.seq:
50: /cgn2_6/ptodata/1/pna/US102A COMB.seq:
51: /cgn2_6/ptodata/1/pna/US102B COMB.seq:
52: /cgn2_6/ptodata/1/pna/US103A COMB.seq:
53: /cgn2_6/ptodata/1/pna/US103B COMB.seq:
54: /cgn2_6/ptodata/1/pna/US104A COMB.seq:
55: /cgn2_6/ptodata/1/pna/US104B COMB.seq:
56: /cgn2_6/ptodata/1/pna/US105A COMB.seq:
57: /cgn2_6/ptodata/1/pna/US105B COMB.seq:
58: /cgn2_6/ptodata/1/pna/US106A COMB.seq:
59: /cgn2_6/ptodata/1/pna/US107A COMB.seq:
60: /cgn2_6/ptodata/1/pna/US107B COMB.seq:
61: /cgn2_6/ptodata/1/pna/US107C COMB.seq:
62: /cgn2_6/ptodata/1/pna/US107D COMB.seq:
63: /cgn2_6/ptodata/1/pna/US108A COMB.seq:
64: /cgn2_6/ptodata/1/pna/US108B COMB.seq:
65: /cgn2_6/ptodata/1/pna/US109A COMB.seq:
66: /cgn2_6/ptodata/1/pna/US109B COMB.seq:
67: /cgn2_6/ptodata/1/pna/US109C COMB.seq:
68: /cgn2_6/ptodata/1/pna/US110 COMB.seq:
69: /cgn2_6/ptodata/1/pna/US6000 COMB.seq:
70: /cgn2_6/ptodata/1/pna/US6001 COMB.seq:
71: /cgn2_6/ptodata/1/pna/US6002 COMB.seq:
72: /cgn2_6/ptodata/1/pna/US6003 COMB.seq:
73: /cgn2_6/ptodata/1/pna/US6004 COMB.seq:
74: /cgn2_6/ptodata/1/pna/US6005 COMB.seq:
75: /cgn2_6/ptodata/1/pna/US6006 COMB.seq:
76: /cgn2_6/ptodata/1/pna/US6007 COMB.seq:
77: /cgn2_6/ptodata/1/pna/US6008 COMB.seq:
78: /cgn2_6/ptodata/1/pna/US6009 COMB.seq:
79: /cgn2_6/ptodata/1/pna/US6010 COMB.seq:
80: /cgn2_6/ptodata/1/pna/US6011 COMB.seq:
81: /cgn2_6/ptodata/1/pna/US6012 COMB.seq:
82: /cgn2_6/ptodata/1/pna/US6013 COMB.seq:
83: /cgn2_6/ptodata/1/pna/US6014 COMB.seq:
84: /cgn2_6/ptodata/1/pna/US6015 COMB.seq:
85: /cgn2_6/ptodata/1/pna/US6016 COMB.seq:
86: /cgn2_6/ptodata/1/pna/US6017 COMB.seq:
87: /cgn2_6/ptodata/1/pna/US6018 COMB.seq:
88: /cgn2_6/ptodata/1/pna/US6019 COMB.seq:
89: /cgn2_6/ptodata/1/pna/US6020 COMB.seq:
90: /cgn2_6/ptodata/1/pna/US6021 COMB.seq:
91: /cgn2_6/ptodata/1/pna/US6022 COMB.seq:
92: /cgn2_6/ptodata/1/pna/US6023A COMB.seq:
93: /cgn2_6/ptodata/1/pna/US6023B COMB.seq:
94: /cgn2_6/ptodata/1/pna/US6024 COMB.seq:
95: /cgn2_6/ptodata/1/pna/US6025 COMB.seq:
96: /cgn2_6/ptodata/1/pna/US6026 COMB.seq:
97: /cgn2_6/ptodata/1/pna/US6027 COMB.seq:
98: /cgn2_6/ptodata/1/pna/US6028 COMB.seq:
99: /cgn2_6/ptodata/1/pna/US6029 COMB.seq:
100: /cgn2_6/ptodata/1/pna/US6030 COMB.seq:
101: /cgn2_6/ptodata/1/pna/US6031 COMB.seq:
102: /cgn2_6/ptodata/1/pna/US6032 COMB.seq:
103: /cgn2_6/ptodata/1/pna/US6033 COMB.seq:
104: /cgn2_6/ptodata/1/pna/US6034 COMB.seq:
105: /cgn2_6/ptodata/1/pna/US6035 COMB.seq:
106: /cgn2_6/ptodata/1/pna/US6036 COMB.seq:
107: /cgn2_6/ptodata/1/pna/US6037 COMB.seq:
108: /cgn2_6/ptodata/1/pna/US6038 COMB.seq:
109: /cgn2_6/ptodata/1/pna/US6039 COMB.seq:
110: /cgn2_6/ptodata/1/pna/US6040 COMB.seq:
111: /cgn2_6/ptodata/1/pna/US6041 COMB.seq:
112: /cgn2_6/ptodata/1/pna/US6042 COMB.seq:
113: /cgn2_6/ptodata/1/pna/US6043 COMB.seq:
114: /cgn2_6/ptodata/1/pna/US6044 COMB.seq:
115: /cgn2_6/ptodata/1/pna/US6045 COMB.seq:
116: /cgn2_6/ptodata/1/pna/US6046 COMB.seq:

Db 661 ACGACTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTTGCAAGAAGACGAAG 840
Db 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTTGCAAGAAGACGAAG 840
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
QY 901 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCATGAGGAG 960
Db 901 GAGGAGGTTGTTTCATCATGATCACAAAGGAACGGGGCTCGTTTATCACCATGAGGAG 960
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTTCAGC 1080
Db 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTTCAGC 1080
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAAGCT 1140
Db 1081 CGCGAAGAGATTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAAGCT 1140
QY 1141 AGTCTC 1146
Db 1141 AGTCTC 1146

RESULT 2

PCT-US02-24567-104
; Sequence 104, Application PC/TUS0224567
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: PCT/US02/24567
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468 *emo*
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24567-104

Query Match 100.0%; Score 1146; DB 1; Length 2005;
Best Local Similarity 100.0%; Pred. No. 4.7e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTTCCGGCCCTGGCCCCGGGCCCGTCTGT 60
Db 66 ATGGCACTGCAGGGCATCTCGGTCTGGAGCTTCCGGCCCTGGCCCCGGGCCCGTCTGT 125
QY 61 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGGCCCGGCTCCCGC 120
Db 126 GCTATGGTCTGGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGGCCCGGCTCCCGC 185
QY 121 TACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180

Db 186 TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGCTGAAGCAGCCG 245
QY 181 CGGGAGCCGCGTGTGTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240
Db 246 CGGGAGCCGCGTGTGTCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 305
QY 241 CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGACGCGGAAATCCA 300
Db 306 CGCCGCGGTGTCTATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGACGCGGAAATCCA 365
QY 301 AGGCTTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 366 AGGCTTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGT 420
Db 426 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAATTTGGCAGAAAGTGT 485
QY 421 GAGAATCCGTATGCCCGCTGAATCTCTCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 480
Db 486 GAGAATCCGTATGCCCGCTGAATCTCTCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 545
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGACCCGACACGCACTGGCAAGGTCAGGTCAAT 540
Db 546 GCACTGGGCATTATAATGGCTCTTTTGGACCCGACACGCACTGGCAAGGTCAGGTCAAT 605
QY 541 GATGCAATATAGTGGAGGAACAGCATATTTAAGTCTTTTCTGGAATACTCAGAAA 600
Db 606 GATGCAATATAGTGGAGGAACAGCATATTTAAGTCTTTTCTGGAATACTCAGAAA 665
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATCATGTTGGATGTTGGAGCACCTTTCTAT 660
Db 666 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATCATGTTGGATGTTGGAGCACCTTTCTAT 725
QY 661 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 726 ACGACTTACAGGACAGCAGATGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 785
QY 721 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 786 TACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 845
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTTGCAAGAAGACGAAG 840
Db 846 ATGGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTAATTTGCAAGAAGACGAAG 905
QY 841 GCAGAGTGGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 900
Db 906 GCAGAGTGGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 965
QY 901 GAGGAGTGGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 960
Db 966 GAGGAGTGGTCAAATCTTTGACGGCACAGATGCTGTGACTCCGGTCTGACTTTT 1025
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTTCAGC 1080
Db 1086 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAAATTGGATTTCAGC 1145
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAAGCT 1140
Db 1146 CGCGAAGAGATTATCAGCTTAACTCAGATATAAATCATTTGAAGTAATAAGGTAAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

```
; Sequence 1, Application US/09967305
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-305-1

Query Match      100.0%; Score 1146; DB 44; Length 2005;
Best Local Similarity 100.0%; Pred. No. 4.7e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGCACTGCAGGGCATCTCGGTCTGGAGCTCCGGCCTGGCCCCGGCCCGTTCGT 60
Db      66  ATGGCACTGCAGGGCATCTCGGTCTGGAGCTCCGGCCTGGCCCCGGCCCGTTCGT 125

QY      61  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC 120
Db      126  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC 185

QY      121  TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
Db      186  TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 245

QY      181  CGGGAGCGCCGCTGCTGGCGCGTCTGTGCAACGGTGGATGTGCTGGAGCCCTTC 240
Db      246  CGGGAGCGCCGCTGCTGGCGCGTCTGTGCAACGGTGGATGTGCTGGAGCCCTTC 305

QY      241  CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 300
Db      306  CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 365

QY      301  AGGCTATTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db      366  AGGCTATTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425

QY      361  GGCCACGATATCAACTATTGGCTTTGTCCAGGTGTCTCTCAAAAATTGGCAGAGTGT 420
Db      426  GGCCACGATATCAACTATTGGCTTTGTCCAGGTGTCTCTCAAAAATTGGCAGAGTGT 485

QY      421  GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGTGGTGGCTTATGTGT 480
Db      486  GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGTGGTGGCTTATGTGT 545

QY      481  GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCA 540
Db      546  GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCA 605

QY      541  GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGMAAACTCAGAAA 600
Db      606  GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGMAAACTCAGAAA 665

QY      601  TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db      666  TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 725

QY      661  ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db      726  ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 785

QY      721  TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db      786  TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 845

QY      781  ATGGATGATTGGCCAGAAATGAAGAAAGTTTTCAGATGTATTTGCAAAAGAACGAAG 840
Db      846  ATGGATGATTGGCCAGAAATGAAGAAAGTTTTCAGATGTATTTGCAAAAGAACGAAG 905

QY      841  GCAGAGTGGTGTCAAATCTTTGACGCGCACAGATGCCTGTGTGACTCCGGTCTGACTTT 900
Db      906  GCAGAGTGGTGTCAAATCTTTGACGCGCACAGATGCCTGTGTGACTCCGGTCTGACTTT 965

QY      901  GAGGAGTGTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db      966  GAGGAGTGTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1025

QY      961  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db      1026  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1085

QY      1021  AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTGAGC 1080
Db      1086  AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTGAGC 1145

QY      1081  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTTGAAAAGTAAGGTAAGGCT 1140
Db      1146  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTTGAAAAGTAAGGTAAGGCT 1205

QY      1141  AGTCTC 1146
Db      1206  AGTCTC 1211
```

```
RESULT 4
US-09-967-305-10
; Sequence 10, Application US/09967305
; GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1211)
US-09-967-305-10

Query Match      100.0%; Score 1146; DB 44; Length 2005;
Best Local Similarity 100.0%; Pred. No. 4.7e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGCACTGCAGGGCATCTCGGTCTGGAGTGTCCGGCCTGGCCCCGGGCCCGTTCGT 60
Db      66  ATGGCACTGCAGGGCATCTCGGTCTGGAGTGTCCGGCCTGGCCCCGGGCCCGTTCGT 125

QY      61  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC 120
Db      126  GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGTACGCGTGGACCGCGCGCTCCCGC 185

QY      121  TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 180
Db      186  TACGACGTGAGCCGCTTGGGCCGGGCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCG 245

QY      181  CGGGAGCGCCGCTGCTGGCGCGTCTGTGCAACGGTGGATGTGCTGGAGCCCTTC 240
Db      246  CGGGAGCGCCGCTGCTGGCGCGTCTGTGCAACGGTGGATGTGCTGGAGCCCTTC 305

QY      241  CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 300
Db      306  CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAATCCA 365

QY      301  AGGCTATTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db      366  AGGCTATTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 425

QY      361  GGCCACGATATCAACTATTGGCTTTGTCCAGGTGTCTCTCAAAAATTGGCAGAGTGT 420
Db      426  GGCCACGATATCAACTATTGGCTTTGTCCAGGTGTCTCTCAAAAATTGGCAGAGTGT 485

QY      421  GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGTGGTGGCTTATGTGT 480
Db      486  GAGAAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGTGGTGGCTTATGTGT 545

QY      481  GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCA 540
Db      546  GCACTGGGCATTATAATGGCTCTTTTGGACCGCACAGCACTGGCAAGGTCAGGTCA 605

QY      541  GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGMAAACTCAGAAA 600
Db      606  GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTCTGTGMAAACTCAGAAA 665

QY      601  TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db      666  TCGAGTCTGTGGGAAGCACTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTCTAT 725

QY      661  ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db      726  ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 785

QY      721  TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db      786  TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGC 845

QY      781  ATGGATGATTGGCCAGAAATGAAGAAAGTTTTCAGATGTATTTGCAAAAGAACGAAG 840
Db      846  ATGGATGATTGGCCAGAAATGAAGAAAGTTTTCAGATGTATTTGCAAAAGAACGAAG 905

QY      841  GCAGAGTGGTGTCAAATCTTTGACGCGCACAGATGCCTGTGTGACTCCGGTCTGACTTT 900
Db      906  GCAGAGTGGTGTCAAATCTTTGACGCGCACAGATGCCTGTGTGACTCCGGTCTGACTTT 965

QY      901  GAGGAGTGTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db      966  GAGGAGTGTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1025

QY      961  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db      1026  CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1085

QY      1021  AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTGAGC 1080
Db      1086  AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAGAAATTTGGATTGAGC 1145

QY      1081  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTTGAAAAGTAAGGTAAGGCT 1140
Db      1146  CGCGAAGAGATTATCAGCTTAACTCAGATAAAAATCATTTGAAAAGTAAGGTAAGGCT 1205

QY      1141  AGTCTC 1146
Db      1206  AGTCTC 1211
```


QY 781 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGACGAAG 840
Db 846 ATGGATGATTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGACGAAG 905
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 906 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 965
QY 901 GAGGAGGTTGTTATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 966 GAGGAGGTTGTTATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1025
QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1026 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1085
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
Db 1086 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1145
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1140
Db 1146 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1205
QY 1141 AGTCTC 1146
Db 1206 AGTCTC 1211

RESULT 6
PCT-US02-23913-17
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044PC
; CURRENT APPLICATION NUMBER: PCT/US02/23913
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-23913-17

Query Match 100.0%; Score 1146; DB 1; Length 2069;
Best Local Similarity 100.0%; Pred. No. 4.8e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTGTGGAGCTGTCGGGCTGGCCCGCGGCGGCTCTGT 60
Db 90 ATGGCACTGCAGGGCATCTCGTGTGGAGCTGTCGGGCTGGCCCGCGGCGGCTCTGT 149
QY 61 GCTATGGTCTGGCTGACTTCGGGCGCGTGTGGTACGCTGGACCGCGCGGCTCCCGC 120
Db 150 GCTATGGTCTGGCTGACTTCGGGCGCGTGTGGTACGCTGGACCGCGCGGCTCCCGC 209
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG 269

QY 181 CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 240
Db 270 CGGGAGCCGCGTGTCTCGGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 329
QY 241 CGCCGCGGTGTATGGAGAAATCCAGCTGGGCCAGAGATTTGACGCGGGAATCCA 300
Db 330 CGCCGCGGTGTATGGAGAAATCCAGCTGGGCCAGAGATTTGACGCGGGAATCCA 389
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 449
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAGTGT 420
Db 450 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAGTGT 509
QY 421 GAGATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 510 GAGATCCGTATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 569
QY 481 GCACTGGGCATTAATATGGCTCTTTTGAACGACACGCACTGGCAAGGTCAGGTCATT 540
Db 570 GCACTGGGCATTAATATGGCTCTTTTGAACGACACGCACTGGCAAGGTCAGGTCATT 629
QY 541 GATGCAATATGTTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 600
Db 630 GATGCAATATGTTGGAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 689
QY 601 TCGAGTCTGTGGAGACACCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTTCTAT 660
Db 690 TCGAGTCTGTGGAGACACCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTTCTAT 749
QY 661 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 750 ACAGCTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 809
QY 721 TACGAGTGTCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 780
Db 810 TACGAGTGTCTGATCAAAAGGACTTGGACTAAAGTCTGATGAATTTCCCAATCAGATGAGC 869
QY 781 ATGGATGTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGACGAAG 840
Db 870 ATGGATGTTGGCCAGAAATGAAGAAGAGTTTGCAGATGTATTTGCAAGAAGACGAAG 929
QY 841 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 989
QY 901 GAGGAGGTTGTTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 990 GAGGAGGTTGTTTCATCATGATCACAAACAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049
QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1080
Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC 1169
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1140
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAAGCT 1229
QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235

RESULT 7
US-09-967-305-4
; Sequence 4, Application US/09967305

GENERAL INFORMATION:
; APPLICANT: Richardson, Jennifer
; APPLICANT: Monahan, John
; TITLE OF INVENTION: METHODS OF USE OF ALPHA-METHYLACYL-CoA RACEMASE IN HORMONE
; TITLE OF INVENTION: REFRACTORY AND METASTATIC PROSTATE CANCERS
; FILE REFERENCE: 07334-312001
; CURRENT APPLICATION NUMBER: US/09/967,305
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,238
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(1235)
US-09-967-305-4

Query Match 100.0%; Score 1146; DB 44; Length 2069;
Best Local Similarity 100.0%; Pred. No. 4.8e-290;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCGGGCTGGCCCGCGGCGCTTCTGT	60
Db	90	ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCGGGCTGGCCCGCGGCGCTTCTGT	149
QY	61	GCTATGCTCTGGCTGCTCGGGGCGCGTGTGTACGCTGGACCGCGCGCTCCCGC	120
Db	150	GCTATGCTCTGGCTGCTCGGGGCGCGTGTGTACGCTGGACCGCGCGCTCCCGC	209
QY	121	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG	180
Db	210	TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGTGTGACCTGAAGCAGCCG	269
QY	181	CGGGAGCGCGCTGCTGGCGCTGTGTCAAGCGGTCGGATGTGCTGGAGCCCTTC	240
Db	270	CGGGAGCGCGCTGCTGGCGCTGTGTCAAGCGGTCGGATGTGCTGGAGCCCTTC	329
QY	241	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGAAATCCA	300
Db	330	CGCCGCGGTGTATGGAGAACTCCAGCTGGGCCACAGAGATTCTGCAGCGGAAATCCA	389
QY	301	AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	360
Db	390	AGGCTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT	449
QY	361	GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCAAAAATTGGCAGAGTGGT	420
Db	450	GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCAAAAATTGGCAGAGTGGT	509
QY	421	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT	480
Db	510	GAGAAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTGTGCTGGTGGCTTATGTGT	569
QY	481	GCACTGGGCATTATAATGGCTTTTGTGACCGCACAGCACTGGCAAGGTCAGGTCAAT	540
Db	570	GCACTGGGCATTATAATGGCTTTTGTGACCGCACAGCACTGGCAAGGTCAGGTCAAT	629
QY	541	GATCAAAATATGGTGAAGGAACAGCATATTAAAGTTCTTTCTGTGAAACTCAGAAA	600
Db	630	GATCAAAATATGGTGAAGGAACAGCATATTAAAGTTCTTTCTGTGAAACTCAGAAA	689
QY	601	TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTCTAT	660
Db	690	TCGAGTCTGTGGGAAGCACTCGAGGACAGAAATGTTGGATGGTGGAGCACTTCTAT	749
QY	661	ACGACTTACAGGACAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCAGTTC	720
Db	750	ACGACTTACAGGACAGATGGGGAATTCATGGCTGTGTGGAGCAATAGAACCCAGTTC	809

QY	721	TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	780
Db	810	TACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC	869
QY	781	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTTCAGATGTATTTGCAAGAGACGAAG	840
Db	870	ATGGATGATTGGCCAGAAATGAAGAAGAGTTTTCAGATGTATTTGCAAGAGACGAAG	929
QY	841	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTGACTTTT	900
Db	930	GCAGAGTGGTGTCAAAATCTTTGACGGCACAGATGCTGTGTGACTCCGGTCTGACTTTT	989
QY	901	GAGGAGGTTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG	960
Db	990	GAGGAGGTTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG	1049
QY	961	CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC	1020
Db	1050	CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC	1109
QY	1021	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC	1080
Db	1110	AAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACCTTGAAGAATTTGGATTTCAGC	1169
QY	1081	CGGAAGAGATTTATCAGCTTAACTCAGATATAATCATTGAAAGTAATAAGTAAAGCT	1140
Db	1170	CGGAAGAGATTTATCAGCTTAACTCAGATATAATCATTGAAAGTAATAAGTAAAGCT	1229
QY	1141	AGTCTC 1146	
Db	1230	AGTCTC 1235	

RESULT 8

US-10-205-823-17
; Sequence 17, Application US/10205823
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-17

Query Match

100.0%; Score 1146; DB 50; Length 2069;

no / late > 2000

QY 1 ATGGCACTGCAGGGCAATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCGGGCCCGTTCTGT 60
Db 90 ATGGCACTGCAGGGCAATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCGGGCCCGTTCTGT 149
QY 61 GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 120
Db 150 GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 209
QY 121 TACGACGTGAGCCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCCG 269
QY 181 CGGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 240
Db 270 CGGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 329
QY 241 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA 300
Db 330 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA 389
QY 301 AGGCTTATTTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 390 AGGCTTATTTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 449
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAAGTGT 420
Db 450 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTCTCTCAAAAATTGGCAGAAAGTGT 509
QY 421 GAGAACTCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 480
Db 510 GAGAACTCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 569
QY 481 GCACTGGCAATTATAATGGCTCTTTTGTACCGCACAGCACTGGCAAGGTCAGGTCAAT 540
Db 570 GCACTGGCAATTATAATGGCTCTTTTGTACCGCACAGCACTGGCAAGGTCAGGTCAAT 629
QY 541 GATGCAAAATATGTTGAAGAAACAGCATATTTAAGTCTTTTCTGTGGAAGAACTCAGAA 600
Db 630 GATGCAAAATATGTTGAAGAAACAGCATATTTAAGTCTTTTCTGTGGAAGAACTCAGAA 689
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTTCTAT 660
Db 690 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAATGTTGGATGTTGGAGCACCTTTCTAT 749
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAATTCATGCTGTTGGAGCAATAGAACCCAGTTC 809
QY 721 TACGAGCTGTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGTGATCAAGAGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 869
QY 781 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAAGACGAAG 840
Db 870 ATGGATGATTGGCCAGAAATGAAGAAGTTTGCAGATGTATTTGCAAGAAAGACGAAG 929
QY 841 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGGTCAAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 989
QY 901 GAGGAGGTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 990 GAGGAGGTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049
QY 961 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1080
Db 1110 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATACCTTGAAGAAATTTGGATTTCAGC 1169
QY 1081 CGCGAAGAGATTTATCAGCTTAACCTCAGATATAAATCATTTGAAAGTAATAAGTAAAAGCT 1140

Db 1170 CGCGAAGAGATTTATCAGCTTAACCTCAGATATAAATCATTTGAAAGTAATAAGTAAAAGCT 1229
QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235
RESULT 13
US-10-205-823-25
; Sequence 25, Application US/10205823
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-25
Query Match 99.9%; Score 1144.4; DB 50; Length 2069;
Best Local Similarity 99.9%; Pred. No. 1.3e-289;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCAATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCGGGCCCGTTCTGT 60
Db 90 ATGGCACTGCAGGGCAATCTCGGTCTGTGGAGCTGTCCGGCCCTGGCCCCGGGCCCGTTCTGT 149
QY 61 GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 120
Db 150 GCTATGGTCTCGGTGACTTTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 209
QY 121 TACGACGTGAGCCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCCG 180
Db 210 TACGACGTGAGCCCGCTTGGGCCGGGCAAGCGCTCGCTAGTGTGCTGGACCTGAAGCAGCCG 269
QY 181 CGGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 240
Db 270 CGGGGAGCCCGCTGCTCGCGCGTCTGTGCAAGCGGTGGATGTGCTGCTGGAGCCCTTC 329
QY 241 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA 300
Db 330 CGCCCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGAAAAATCCA 389
QY 301 AGGCTTATTTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360

file > 7000

Db 390 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 449
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 450 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGT 509
QY 421 GAGAAATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTTG 480
Db 510 GAGAAATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGTGGCTTATGTTG 569
QY 481 GCACATGGGCAATATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
Db 570 GCACATGGGCAATATAATGGCTCTTTTGGACCGCACACGCACTGGCAAGGTCAGGTCAAT 629
QY 541 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTCAGAAA 600
Db 630 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTCAGAAA 689
QY 601 TCGAGTCTGTGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCAT 660
Db 690 TCGAGTCTGTGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCAT 749
QY 661 ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 720
Db 750 ACGACTTACAGGACAGCAGATGGGGAAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 809
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 810 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC 869
QY 781 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTAATTTGCAAAAGAACGAAAG 840
Db 870 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTAATTTGCAAAAGAACGAAAG 929
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 930 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 989
QY 901 GAGGAGGTTGTTTCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 990 GAGGAGGTTGTTTCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 1049
QY 961 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1020
Db 1050 CAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCGCCATCCCTTCTTTC 1109
QY 1021 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
Db 1110 AAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1169
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1140
Db 1170 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1229
QY 1141 AGTCTC 1146
Db 1230 AGTCTC 1235

RESULT 14
US-60-324-185-30337
; Sequence 30337, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862

; SOFTWARE: PERL Program
; SEQ ID NO 30337
; LENGTH: 3066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 441227.2
US-60-324-185-30337

Query Match 99.9%; Score 1144.4; DB 102; Length 3066;
Best Local Similarity 99.9%; Pred. No. 1.5e-289;
Matches 1145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCCGCTTCTGT 60
Db 92 ATGGCACTGCAGGGCATCTCGTCTGTGGAGCTGTCCGGCCTGGCCCCGGCCCGCTTCTGT 151
QY 61 GCTATGCTCTGGCTGACTTCGGGGCGCGTGTGGTACCGGTGAGACCGGCCCGCTCCCGC 120
Db 152 GCTATGCTCTGGCTGACTTCGGGGCGCGTGTGGTACCGGTGAGACCGGCCCGCTCCCGC 211
QY 121 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
Db 212 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 271
QY 181 CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 240
Db 272 CGGGAGCCCGCTGCTCGGGCGTCTGTGCAAGCGGTCCGATGTGCTGGAGCCCTTC 331
QY 241 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAAATCCA 300
Db 332 CGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCGAGAGATTCGACGCGGGAAATCCA 391
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360
Db 392 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 451
QY 361 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 452 GGCCACGATATCAACTATTGGCTTTGTGAGGTGTTCTCTCAAAAATTTGGCAGAAAGTGGT 511
QY 421 GAGAAATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTATGTTG 480
Db 512 GAGAAATCCGATATGCCCGCTGAATCTCTGGCTGACTTTGCTGGTGGCTTATGTTG 571
QY 481 GCACATGGGCAATTAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 540
Db 572 GCACATGGGCAATTAATGGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGGTCAAT 631
QY 541 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTCAGAAA 600
Db 632 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTTCTGTGAAAACTCAGAAA 691
QY 601 TCGAGTCTGTGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCAT 660
Db 692 TCGAGTCTGTGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCAT 751
QY 661 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 720
Db 752 ACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAAACCCAGTTC 811
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC 780
Db 812 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCAATCAGATGAGC 871
QY 781 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTAATTTGCAAAAGAACGAAAG 840
Db 872 ATGGATGATTGGCCAGAAAATGAAGAAGATTGTCAGATGTAATTTGCAAAAGAACGAAAG 931
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 932 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 991

ca 720 30

QY 901 GAGGAGGTTGTTTCATCATGATCAACAAGAAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 992 GAGGAGGTTGTTTCATCATGATCAACAAGAAACGGGGCTCGTTTATCACCAGTGAGGAG 1051
QY 961 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1020
Db 1052 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTC 1111
QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1080
Db 1112 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1171
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1140
Db 1172 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1231
QY 1141 AGTCTC 1146
Db 1232 AGTCTC 1237

RESULT 15

PCT-US02-14753A-107
; Sequence 107, Application PC/TUS0214753A

GENERAL INFORMATION:

; APPLICANT: Corixa Corporation
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42725PC

; CURRENT APPLICATION NUMBER: PCT/US02/14753A

; CURRENT FILING DATE: 2002-05-09

; NUMBER OF SEQ ID NOS: 1033

; SOFTWARE: FASTA/SEQ for Windows Version 3.0

; SEQ ID NO 107

; LENGTH: 1621

; TYPE: DNA

; ORGANISM: Homo sapiens

PCT-US02-14753A-107

Query Match 99.7%; Score 1142.8; DB 1; Length 1621;
Best Local Similarity 99.8%; Pred. No. 3e-289;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGGTGAGCTGTCGGCCCTGGCCCGCGCGCTTCTGT 60

Db 5 ATGGCACTGCAGGGCATCTCGGTGAGCTGTCGGCCCTGGCCCGCGCGCTTCTGT 64

QY 61 GCTATGGTCTGGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGCCCGCTCCCGC 120

Db 65 GCTATGGTCTGGCTGACTTCGGGGCGGTGTGGTACGGTGGACCGGCCCGCTCCCGC 124
QY 121 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTAGTGTGACCTGAGCAGCAGCG 180
Db 125 TACGACGTGAGCCGCTTGGCCCGGGCAAGCGCTAGTGTGACCTGAGCAGCAGCG 184
QY 181 CGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCGGATGTGCTGAGAGCCCTTC 240
Db 185 CGGGAGCCCGCTGCTGCGGCGTCTGTGCAAGCGGTCGGATGTGCTGAGAGCCCTTC 244
QY 241 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGSCCCAGAGATTCTGCAGCGGGGAAATCCA 300
Db 245 CGCCGCGGTGTCATGGAGAAACTCCAGCTGGSCCCAGAGATTCTGCAGCGGGGAAATCCA 304
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 360
Db 305 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 364
QY 361 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGGT 420
Db 365 GGCCACGATATCAACTATTTGGCTTTGTGAGTGTCTCTCAAAAATTTGGCAGAAAGTGGT 424
QY 421 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 480
Db 425 GAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGTGCTGGTGGCTTATGTGT 484
QY 481 GCACTGGGCATTATAATGGCTCTTTTACCCGACACGACCTGGCAAGGCTCAGGTCATT 540
Db 485 GCACTGGGCATTATAATGGCTCTTTTACCCGACACGACCTGGCAAGGCTCAGGTCATT 544
QY 541 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAACTCAGAAA 600
Db 545 GATGCAAAATATGGTGGAAAGAACAGCATATTTAAGTTCTTTTCTGTGGAAACTCAGAAA 604
QY 601 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 605 TCGAGTCTGTGGAAAGCACCTCGAGGACAGAAATGTTGGATGGTGGAGCACCTTTCTAT 664
QY 661 ACAGCTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 665 ACAGCTTACAGGACAGCAGATGGGAAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 724
QY 721 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 725 TACGAGCTGCTGATCAAAAGGACTTGGACTTAAAGTCTGATGAACCTCCCAATCAGATGAGC 784
QY 781 ATGGATGATTGCCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAGAAGACGAAG 840
Db 785 ATGGATGATTGCCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAGAAGACGAAG 844
QY 841 GCAGAGTGTGTCAAATCTTTGACCGGACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 845 GCAGAGTGTGTCAAATCTTTGACCGGACAGATGCCCTGTGTGACTCCGGTTCTGACTTTT 904
QY 901 GAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 960
Db 905 GAGGAGGTTGTTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAG 964
QY 961 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db 965 CAGGACGTGAGCCCCCGCTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1024
QY 1021 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1080
Db 1025 AAAAGGGATCCTTTTCATAGGAGAAACACACTGAGGAGATCTTGAAGAATTTGGATTTCAGC 1084
QY 1081 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1140
Db 1085 CGCGAAGAGATTATCAGCTTAACTCAGATAAAATCATTTGAAAGTAATAAGTAAAGCT 1144
QY 1141 AGTCTC 1146

Db 1145 AGTCTC 1150

Search completed: July 27, 2005, 10:25:21
Job time : 5005 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:00:01 ; Search time 4256 Seconds
(without alignments)
10249.448 Million cell updates/sec

Title: US-09-967-305-3
Perfect score: 1146
Sequence: 1 atggcactgcaggcatctc.....ataaggtaaaagctagtctc 1146

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044	91.1	1544	3	CR615811 full-leng
2	1044	91.1	1967	3	CR625004 full-leng
3	1044	91.1	3111	3	CR616479 full-leng
4	762	66.5	977	1	AL558928 AL558928
5	664	57.9	890	5	BQ962523 AGENCOURT
6	635	55.4	955	4	BG741165 602631843
7	601	52.4	1081	1	AL545355
8	589	51.4	649	5	BQ638373 hd21909.Y
9	572	49.9	808	4	BI256255 602975075
10	572	49.9	893	1	AL558977 AL558977
11	568	49.6	622	7	CN305057 BQ941482
12	567	49.5	890	5	BQ941482 AGENCOURT
13	562	49.0	613	7	CN305056 CN305056
14	561	49.0	812	4	BG035606 BG035606
15	552	48.2	583	5	BP318564 BP318564
16	552	48.2	1598	3	CR618063 full-leng
17	534	46.6	633	5	BX099124 BX099124
18	530	46.2	935	4	BG286300 602382457
19	528	46.1	880	4	BG289921 602381336
20	524	45.7	720	1	AU117376 AU117376
21	519	45.3	1076	1	AL555978 AL555978
22	507	44.2	713	1	AV714764 AV714764
23	501	43.7	583	5	BP275107 BP275107
24	498	43.5	729	4	BI550368 603192419

25	498	43.5	871	5	BX449005	BX449005 BX449005
26	468	40.8	588	5	BP239487	BP239487 BP239487
27	460	40.1	693	4	BG779839	BG779839 602667316
28	456	39.8	958	5	BX390793	BX390793 BX390793
29	436	38.0	581	5	BP276627	BP276627 BP276627
30	435	38.0	582	5	BP221988	BP221988 BP221988
31	434	37.9	582	5	BP199866	BP199866 BP199866
32	432	37.7	583	5	BP260668	BP260668 BP260668
33	429	37.4	451	7	CF142100	CF142100 UI-HF-CB0
34	403	35.2	805	6	CD643323	CD643323 AGENCOURT
35	396	34.6	585	5	BP261417	BP261417 BP261417
36	394	34.4	530	7	CN305058	CN305058 170006000
37	394	34.4	705	4	BI597403	BI597403 603243613
38	394	34.4	829	4	BG708726	BG708726 602674280
39	393	34.3	641	4	BM829952	BM829952 K-EST0103
40	393	34.3	677	6	CB268128	CB268128 1007034 H
41	391	34.1	672	4	BM714377	BM714377 UI-E-EJ0-
42	391	34.1	823	4	BM723657	BM723657 UI-E-EJ0-
43	386	33.7	938	2	BE622419	BE622419 601441213
44	385	33.6	943	4	BG289079	BG289079 602383954
45	383	33.4	581	5	BP311844	BP311844 BP311844

ALIGNMENTS

RESULT 1
CR615811
LOCUS CR615811 1544 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI027YJ12 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR615811
VERSION CR615811.1 GI:50496618
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1544)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitroGen Corporation 1600 Faraday Avenue
2 (bases 1 to 1544)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
Location/Qualifiers
1..1544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI027YJ12"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 91.1%; Score 1044; DB 3; Length 1544;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGCATCTCGGTCTGGTGGAGCTGTCGGCCTGGCCCCCGGTCGTTCTGT 60
|||||
Db 10 ATGGCACTGCAGGCATCTCGGTCTGGTGGAGCTGTCGGCCTGGCCCCCGGTCGTTCTGT 69

QY 61 GCTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACCGGTGGACCGGCCCGGCTCCCGC 120
Db |||||||
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
Db |||||||
QY 130 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 189
Db |||||||
QY 181 CGGGAGCCGCGTGTCTGCGGCTCTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 240
Db |||||||
QY 190 CGGGAGCCGCGTGTCTGCGGCTCTGTGCAAGCGGTGGATGTCTGCTGGAGCCCTTC 249
Db |||||||
QY 241 CGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||||
QY 250 CGCGCGGTGTCTATGGAGAACTCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 309
Db |||||||
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGCTTAGCT 360
Db |||||||
QY 310 AGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAAGAACTTCTGCCGCTTAGCT 369
Db |||||||
QY 361 GGCCAGCATATCAACTATTGGCTTTGTCAAGTGTCTCTCAAAAATTGGCAGAAGTGGT 420
Db |||||||
QY 421 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGCTTATGTGT 480
Db |||||||
QY 430 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGTGGTGGCTTATGTGT 489
Db |||||||
QY 481 GCACTGGGCATTATAATGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGTCAAT 540
Db |||||||
QY 490 GCACTGGGCATTATAATGCTCTTTTGACCGCACACGCACTGGCAAGGTCAGTCAAT 549
Db |||||||
QY 541 GATCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTCTGTGGAACCTCAGAAA 600
Db |||||||
QY 550 GATGCAAAATATGTTGGAAGGAACAGCATATTTAAAGTTCTTTCTGTGGAACCTCAGAAA 609
Db |||||||
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 660
Db |||||||
QY 610 TTGAGTCTGTGGGAAGCACCTCGAGGACAGAAACATGTTGGATGGTGGAGCACCTTCTAT 669
Db |||||||
QY 661 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 720
Db |||||||
QY 670 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTGGAGCAATAGAACCCAGTTC 729
Db |||||||
QY 721 TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGTAGTAACTTCCCAATCAGATGAGC 780
Db |||||||
QY 730 TACGAGCTGTGATCAAAGGACTTGGACTAAAGTCTGTAGTAACTTCCCAATCAGATGAGC 789
Db |||||||
QY 781 ATGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGCAAAAGAGACGAAG 840
Db |||||||
QY 790 ATGATGATTGGCCAGAAATGAAGAAGATTGTCAGATGTATTTGTCAGAGAGACGAAG 849
Db |||||||
QY 841 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db |||||||
QY 850 GCAGATGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 909
Db |||||||
QY 901 GAGAGGTTGTTTCATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACAGTGAGGAG 960
Db |||||||
QY 910 GAGAGGTTGTTTCATCATGATCACAACAAAGGAACGGGGCTCGTTTATCACAGTGAGGAG 969
Db |||||||
QY 961 CAGGAGTGAGCCCCCGCTTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1020
Db |||||||
QY 970 CAGGAGTGAGCCCCCGCTTGACCTCTGCTGTTAAACACCCAGCCATCCCTTCTTTC 1029
Db |||||||
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1080
Db |||||||
QY 1030 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAAATTTGGATTTCAGC 1089
Db |||||||
QY 1081 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAATAAGGTAAAGCT 1140
Db |||||||
QY 1090 CGCGAAGAGATTTTATCAGCTTAACTCAGATAAAATCATTTGAAAAGTAATAAGGTAAAGCT 1149
Db |||||||

QY 1141 AGTCTC 1146
Db 1150 AGTCTC 1155

RESULT 2
CR625004
LOCUS
DEFINITION CR625004 1967 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DJ007YI07 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
ACCESSION CR625004
VERSION CR625004.1 GI:50505811
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1967)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 1967)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
Location/Qualifiers
source
1..1967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ007YI07"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 91.1%; Score 1044; DB 3; Length 1967;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCCGGCCCTGGCCCCCGGCTTCTGT 60
Db |||||||
QY 45 ATGGCACTGCAGGGCATCTCGTCTGGAGCTGTCCGGCCCTGGCCCCCGGCTTCTGT 104
Db |||||||
QY 61 GCTATGGTCTCGTGAATTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 120
Db |||||||
QY 105 GCTATGGTCTCGTGAATTCGGGGCGCGTGTGTACGCGTGGACCGGCCCGCTCCCGC 164
Db |||||||
QY 121 TACGACGTGAGCCGTTGGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 180
Db |||||||
QY 165 TACGACGTGAGCCGTTGGGCCCGGGCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCG 224
Db |||||||
QY 181 CGGGAGCCCGCTGTCTGCGGCGTCTGTGCAACGGGTGGATGTGCTGTGAGCCCTTC 240
Db |||||||
QY 225 CGGGAGCCCGCTGTCTGCGGCGTCTGTGCAACGGGTGGATGTGCTGTGAGCCCTTC 284
Db |||||||
QY 241 CGCCCGGTGTCTATGGAGAAAATCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 300
Db |||||||
QY 285 CGCCCGGTGTCTATGGAGAAAATCCAGCTGGGCCAGAGATTCTGCAGCGGGAATCCA 344
Db |||||||
QY 301 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 360
Db |||||||
QY 345 AGGCTTATTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGCTTAGCT 404
Db |||||||

QY 361 GGCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420
Db 405 GGCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 464
QY 421 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGGTGGTGGTGGTGGTGGTGGT 480
Db 465 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGGTGGTGGTGGTGGTGGTGGT 524
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCTGGCAAGGGTCAGGTCAATT 540
Db 525 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCTGGCAAGGGTCAGGTCAATT 584
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 600
Db 585 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 644
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 645 TTGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 704
QY 661 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 720
Db 705 ACGACTTACAGGACAGCATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCAGTTC 764
QY 721 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 780
Db 765 TACGAGCTGCTGATCAAGGACTTGGACTAAAGTCTGATGAACCTCCCAATCAGATGAGC 824
QY 781 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 840
Db 825 ATGATGATTTGGCCAGAAATGAAGAAGATTGTCAGATGATTTGCAAGAAGACGAAG 884
QY 841 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 900
Db 885 GCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTT 944
QY 901 GAGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 960
Db 945 GAGAGGTTGTTTCATCATGATCAACAAGGAACGGGGCTCGTTTATCACCAGTGAAGAG 1004
QY 961 CAGGAGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTTC 1020
Db 1005 CAGGAGTGAGCCCCCGCTGCACCTCTGCTGTTAAACACCCCGAGCCATCCCTTCTTTC 1064
QY 1021 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTGAGC 1080
Db 1065 AAAAGGATCCTTTTCATAGGAGAACACACTGAGGAGATCTTGAAGAATTTGGATTGAGC 1124
QY 1081 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATGAAGTAATAAGGTAAAGCT 1140
Db 1125 CGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCAATGAAGTAATAAGGTAAAGCT 1184
QY 1141 AGTCTC 1146
Db 1185 AGTCTC 1190

RESULT 3
CR616479
LOCUS CR616479 3111 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DK010Y111 of HeLa cells Cot 25-normalized of Homo sapiens (human).
ACCESSION CR616479
VERSION CR616479.1 GI:50497286
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 3111)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source
1..3111
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK010Y111"
/tissue type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 91.1%; Score 1044; DB 3; Length 3111;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1144; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGGCTGGCCCCGGCCCGTTCGT 60
Db 77 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGGCTGGCCCCGGCCCGTTCGT 136
QY 61 GCTATGGTCTGGTGAATTCGGGGCGCGTGTGTACGCGTGGACCGGCGCGGCTCCCGC 120
Db 137 GCTATGGTCTGGTGAATTCGGGGCGCGTGTGTACGCGTGGACCGGCGCGGCTCCCGC 196
QY 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGTCTGCTAGTGTGGACCTGAAGCAGCG 180
Db 197 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGTCTGCTAGTGTGGACCTGAAGCAGCG 256
QY 181 CGGGAGCGCGCGCTGCTGCGGCGCTGTGTCAAGCGTGGATGTGCTGGAGCCCTTC 240
Db 257 CGGGAGCGCGCGCTGCTGCGGCGCTGTGTCAAGCGTGGATGTGCTGGAGCCCTTC 316
QY 241 CGCCCGGCTGTCATGGAGAAACTCCAGCTGGGCGCCAGAGATTCTGCAGCGGGGAAATCCA 300
Db 317 CGCCCGGCTGTCATGGAGAAACTCCAGCTGGGCGCCAGAGATTCTGCAGCGGGGAAATCCA 376
QY 301 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCAGTCAAGAGCTTCTGCCGGTTAGCT 360
Db 377 AGGCTTATTTATGCCAGGCTGAGTGGATTTGGCAGTCAAGAGCTTCTGCCGGTTAGCT 436
QY 361 GGCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 420
Db 437 GGCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGCAGAGTGGT 496
QY 421 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGGTGGTGGTGGTGGTGGTGGT 480
Db 497 GAGATCCGTATGCCCGCTGAATCTCTGGCTGACTTTGGTGGTGGTGGTGGTGGTGGT 556
QY 481 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCTGGCAAGGGTCAGGTCAATT 540
Db 557 GCACTGGGCATTATAATGGCTCTTTTGGCCGACACGCTGGCAAGGGTCAGGTCAATT 616
QY 541 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 600
Db 617 GATGCAAAATATGGTGAAGGAACAGCATATTTAAGTTCCTTTCTGTGGAATACTCAGAAA 676
QY 601 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 660
Db 677 TCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTAT 736

DEFINITION AGENCOURT 8817570 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6379327
5', mRNA sequence.
ACCESSION BQ962523
VERSION BQ962523.1 GI:22378001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2566 row: c column: 08
High quality sequence stop: 750.
FEATURES
source
1..890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6379327"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
Note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
ORIGIN
Query Match 57.9%; Score 664; DB 5; Length 890;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 714; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 TGGAGCTGCCGCTGGCCCGCCCGCTTCTGTCTATGTCCTGGCTGACTTCGGGG 85
DB 68 TGGAGCTGCCGCTGGCCCGCCCGCTTCTGTCTATGTCCTGGCTGACTTCGGGG 127
QY 86 CGCGTGTGTACGCGTGGACCGCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGCCCGG 145
DB 128 CGCGTGTGTACGCGTGGACCGCGCCCGCTCCCGCTACGACGTGAGCCGCTTGGCCCGG 187
QY 146 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGAGCCCGCTGTGCTGCGGCGTC 205
DB 188 GCAAGCGCTCGTAGTGTGGACCTGAAGCAGCCCGGGAGCCCGCTGTGCTGCGGCGTC 247
QY 206 TGTCAAGCGGTGGATGTGCTGTGGAGCCCTTCCGCGCGGTGTGTCATGGAGAACTCC 265
DB 248 TGTCAAGCGGTGGATGTGCTGTGGAGCCCTTCCGCGCGGTGTGTCATGGAGAACTCC 307
QY 266 AGCTGGGCCCAGAGATTCTGCAGCGGGGAAATCCAAAGCTTATTATGCCAGGTGAGTG 325
DB 308 AGCTGGGCCCAGAGATTCTGCAGCGGGGAAATCCAAAGCTTATTATGCCAGGTGAGTG 367
QY 326 GATTGGCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTT 385
DB 368 GATTGGCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTT 427
QY 386 TGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGCTATGCCCGCTGAATC 445

DB 428 TGTCAAGTGTCTCTCAAAAATTGGCAGAAAGTGGTGAGAAATCCGCTATGCCCGCTGAATC 487
QY 446 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTAATGGCTCTTT 505
DB 488 TCCTGGCTGACTTTGCTGGTGGTGGCCCTTATGTGTGCACTGGGCATTAATGGCTCTTT 547
QY 506 TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGAACAG 565
DB 548 TTGACCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGAACAG 607
QY 566 CATATTAAAGTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 625
DB 608 CATATTAAAGTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTGGAAAGCACCTCGAG 667
QY 626 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 685
DB 668 GACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGG 727
QY 686 AATTCAATGGCTGTGGAGCAATAGAACCCAGTCTTACGAGTCTGTGATCAAAG 740
DB 728 AATTCAATGGCTGTGGAGCAATAGAACCCAGTCTTACGAGTCTGTGATCAAAG 782
RESULT 6
BG741165
LOCUS BG741165
DEFINITION 602631843F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776971 5',
mRNA sequence.
ACCESSION BG741165
VERSION BG741165.1 GI:14051818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10630 row: f column: 12
High quality sequence stop: 805.
FEATURES
source
1..955
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4776971"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 55.4%; Score 635; DB 4; Length 955;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 785; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 150 GCGCTCGCTAGTGTGGACTGAAGCAGCCCGGGAGCCCGCTGCTGCGGCTGTGTG 209
DB 1 GCGCTCGCTAGTGTGGACTGAAGCAGCCCGGGAGCCCGCTGCTGCGGCTGTGTG 60


```
Qy 210 CAAGCGTGGATGTGCTGTGAGCCCTTCCGCCGGGTGTCTATGGAGAACTCAGCT 269
Db 61 CAAGCGTGGATGTGCTGTGAGCCCTTCCGCCGGGTGTCTATGGAGAACTCAGCT 120

Qy 270 GGGCCAGAGATTCTGCAGCGGGAANAATCCAAGGCTTATTATGCCAGGCTGAGTGGATT 329
Db 121 GGGCCAGAGATTCTGCAGCGGGAANAATCCAAGGCTTATTATGCCAGGCTGAGTGGATT 180

Qy 330 TGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 389
Db 181 TGGCCAGTCAGGAAGCTTCTGCCGTTAGCTGGCCACGATATCAACTATTTGGCTTTGTC 240

Qy 390 AGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAAATCCGTATGCCCCCGCTGAATCTCCT 449
Db 241 AGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAAATCCGTATGCCCCCGCTGAATCTCCT 300

Qy 450 GGCTGACTTTGCTGGTGGCTTATGTGCACTGGGCATTATAATGGCTCTTTTGA 509
Db 301 GGCTGACTTTGCTGGTGGCTTATGTGCACTGGGCATTATAATGGCTCTTTTGA 360

Qy 510 CCGCACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACACAGCATA 569
Db 361 CCGCACGCACTGGCAAGGTCAGGTCATTGATGCAAAATATGGTGGAGGAACACAGCATA 420

Qy 570 TTTAAGTCTTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 629
Db 421 TTTAAGTCTTTTCTGTGGAAAACCTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 480

Qy 630 GAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGAAATT 689
Db 481 GAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGAAATT 540

Qy 690 CATGGCTGTTGGAGCAATAGAACCCCAAGTTCTACGAGCTGCTGATCAAAGGACTTGGACT 749
Db 541 CATGGCTGTTGGAGCAATAGAACCCCAATTTCTACGAGCTGCTGATCAAAGGACTTGGACT 600

Qy 750 AAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGATGGCCAGAAATGAAGAAGAA 809
Db 601 AAAGTCTGATGAACCTTCCCAATCAGATGAGCATGGATGGATGGCCAGAAATGAAGAAGAA 660

Qy 810 GTTTGCAGATGTATTTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCAC 869
Db 661 GTTTGCAGATGTATTTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCAC 720

Qy 870 AGATGCCTGTGACTCCGGTCTTGACTTTTGAGGAGGTGTTTCATCATGATCACAACAA 929
Db 721 AGATGCCTGTGACTCCGGTCTTGACTTTTGAGGAGGTGTTTCATCATGATCACAACAA 780

Qy 930 GGAACGGG 937
Db 781 GGAACGGG 788
```

```
RESULT 7
AL545355
LOCUS
DEFINITION
AL545355 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI027YJ12 5-PRIME, mRNA sequence.
ACCESSION
AL545355
VERSION
AL545355.3 GI:45745838
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1081)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:31267191.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
```

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2801.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DI027DE06QP1&c=2801.r>.

FEATURES
source

1..1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI027YJ12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 52.4%; Score 601; DB 1; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCACTGCAGGCATCTCGGTGCTGGAGCTGTCCGGCCCTGGCCCCGGCCGCTTCTGT 60
Db 10 ATGGCACTGCAGGCATCTCGGTGCTGGAGCTGTCCGGCCCTGGCCCCGGCCGCTTCTGT 69

Qy 61 GCTATGGTCCTGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGCCCGCTCCCGC 120
Db 70 GCTATGGTCCTGCTGACTTCGGGGCGCGTGTGCTACGCGTGGACCGCCCGCTCCCGC 129

Qy 121 TAGCACGTGAGCCGCTTGGGGCGGGCAAGCGTCTGCTAGTCTGGACCTGAAGCAGCCG 180
Db 130 TAGCACGTGAGCCGCTTGGGGCGGGCAAGCGTCTGCTAGTCTGGACCTGAAGCAGCCG 189

Qy 181 CGGGAGCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 240
Db 190 CGGGAGCCGCTGCTGCGGCGTCTGTGCAAGCGGTGGATGTGCTGGAGCCCTTC 249

Qy 241 CGCCGCGGTGTCATGGAGAAAACCTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA 300
Db 250 CGCCGCGGTGTCATGGAGAAAACCTCCAGCTGGGCCCCAGAGATTCTGCAGCGGAAAAATCCA 309

Qy 301 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 360
Db 310 AGGCTTATTTATGCCAGGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGTTAGCT 369

Qy 361 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAAATTGGCAGAAAGTGGT 420
Db 370 GGCCACGATATCAACTATTTGGCTTTGTGAGGTGTTCTCAAAAAATTGGCAGAAAGTGGT 429

Qy 421 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 480
Db 430 GAGAAATCCGATATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGCTTATGTGT 489

Qy 481 GCACCTGGGCATTATAATGGCTCTTTTGGACCGCACACGACTGGCAAGGTCAGGTCAATT 540
Db 490 GCACCTGGGCATTATAATGGCTCTTTTGGACCGCACACGACTGGCAAGGTCAGGTCAATT 549

Qy 541 GATGCAAAATATGGTGAAGGAACAGCATAATTTAAAGTTCTTTTCTGTGGAAAACTCAGAAA 600
Db 550 GATGCAAAATATGGTGAAGGAACAGCATAATTTAAAGTTCTTTTCTGTGGAAAACTCAGAAA 609

Qy 601 T 601
Db 610 T 610

BQ638373
LOCUS
DEFINITION BQ638373 649 bp mRNA linear EST 15-JUL-2002
hd21g09.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
Homo sapiens cDNA clone hd21g09 5', mRNA sequence.
ACCESSION BQ638373
VERSION BQ638373.1 GI:21762832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE 22103461
PUBMED 12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 21 row: g column: 09
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd21g09"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTTCTAGTCGCGAGCGCGGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
ORIGIN
Query Match 51.4%; Score 589; DB 5; Length 649;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 639; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 150 GCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGAGCGCGGTGCTCGGGCTGTGTG 209
|||||
Db 10 GCGCTCGCTAGTGTGGACCTGAAGCAGCCCGGGAGCGCGGTGCTCGGGCTGTGTG 69
Qy 210 CAAGCGGTGGATGTGCTGTGGAGCCCTTCCGCCCGCGGTGCATGGAGAACTCCAGCT 269
|||||
Db 70 CAAGCGGTGGATGTGCTGTGGAGCCCTTCCGCCCGCGGTGCATGGAGAACTCCAGCT 129
Qy 270 GGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTATGCCAGGCTGAGTGGATT 329
|||||
Db 130 GGGCCCCAGAGATTCTGCAGCGGGGAAATCCAAAGGCTTATTATGCCAGGCTGAGTGGATT 189
Qy 330 TGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTTTGTC 389

Db 190 TGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTGGCTTTGTC 249
Qy 390 AGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATCCCCCGCTGAATCTCCT 449
|||||
Db 250 AGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATCCCCCGCTGAATCTCCT 309
Qy 450 GGCTGACTTTTGTGGTGGTGGCCTTATGTGTGACTGGGCATTATAATGGCTCTTTTGA 509
|||||
Db 310 GGCTGACTTTTGTGGTGGTGGCCTTATGTGTGACTGGGCATTATAATGGCTCTTTTGA 369
Qy 510 CCGCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAGCATA 569
|||||
Db 370 CCGCACACGCACTGACAAGGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAGCATA 429
Qy 570 TTTAAGTTCTTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 629
|||||
Db 430 TTTAAGTTCTTTTCTGTGGAAGAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACA 489
Qy 630 GAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGGAATT 689
|||||
Db 490 GAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGGAATT 549
Qy 690 CATGGCTGTTGGAGCAATAGAACCCCGAGTCTTACGAGCTGCTGATCAAAGGACTTGGACT 749
|||||
Db 550 CATGGCTGTTGGAGCAATAGAACCCCGAGTCTTACGAGCTGCTGATCAAAGGACTTGGACT 609
Qy 750 AAAGTCTGATGAACCTCCCAATCAGATGAGCATGGATGAT 789
|||||
Db 610 AAAGTCTGATGAACCTCCCAATCAGATGAGCATGGATGAT 649
RESULT 9
BI256255
LOCUS
DEFINITION BI256255 808 bp mRNA linear EST 17-JUL-2001
602975075F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114130 5',
mRNA sequence.
ACCESSION BI256255
VERSION BI256255.1 GI:14810488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11277 row: f column: 19
High quality sequence stop: 751.
Location/Qualifiers
1. .808
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5114130"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
FEATURES
source
ORIGIN

Dbb 61 CTTTGCTGGTGGCCCTTATGTGTGCACTGGGCATTATAATGGCTCTTTTGTACCGCAC 120

Qy 516 ACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGTGGAAGGAACAGCAVATTTAAG 575

Dbb 121 ACGCACTGGCAAGGGTCAGGTCAATTGATGCAAAATATGTGGAAGGAACAGCATATTTAAG 180

Qy 576 TTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACAT 635

Dbb 181 TTCTTTTCTGTGGAAAACTCAGAAATGAGTCTGTGGGAAGCACCTCGAGGACAGAACAT 240

Qy 636 GTTGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGGAATTCATGGC 695

Dbb 241 GTTGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGGAATTCATGGC 300

Qy 696 TGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTC 755

Dbb 301 TGTGGAGCAATAGAACCCCGAGTTCTACGAGCTGCTGATCAAAAGGACTTGGACTAAAGTC 360

Qy 756 TGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAAAATGAAGAAGAGTTTGC 815

Dbb 361 TGATGAACCTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAAAATGAAGAAGAGTTTGC 420

Qy 816 AGATGTATTTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGC 875

Dbb 421 AGATGTATTTGCAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGC 480

Qy 876 CTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACG 935

Dbb 481 CTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACG 540

Qy 936 GGGTCGTTTATCACCAGTGAGGACGAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTT 995

Dbb 541 GGGTCGTTTATCACCAGTGAGGACGAGACGTGAGCCCCCGCCCTGCACCTCTGCTGTT 600

Qy 996 AAACACCCCGCCATCCC 1013

Dbb 601 AAACACCCCGCCATCCC 618

RESULT 13

CN305056

LOCUS CN305056 613 bp mRNA linear EST 16-MAY-2004

DEFINITION 1700531862255 GRN_ES Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN305056

VERSION CN305056.1 GI:47321470

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.

TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 613 Std Error: 0.00.
Location/Qualifiers

FEATURES

source 1. .613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN_ES"

/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 49.0%; Score 562; DB 7; Length 613;
Best Local Similarity 99.8%; Pred. No. 5.1e-302;
Matches 612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 GAGCTGTCCGGCTGGCCCCCGGCCCGTTCTGTGCTATGGTCTCTGGCTGACTTCGGGGCG 87

Dbb 1 GAGCTGTCCGGCTGGCCCCCGGCCCGTTCTGTGCTATGGTCTCTGGCTGACTTCGGGGCG 60

Qy 88 CGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGTTGGGCCGGGGC 147

Dbb 61 CGTGTGTACGCGTGGACCGGCCCGGCTCCCGCTACGACGTGAGCCGTTGGGCCGGGGC 120

Qy 148 AAGCGCTCGCTAGTGTGACCTGAAGCAGCCGCGGGGAGCCCGCTGCTGCGGCGTCTG 207

Dbb 121 AAGCGCTCGCTAGTGTGACCTGAAGCAGCCGCGGGGAGCCCGCTGCTGCGGCGTCTG 180

Qy 208 TGCAAGCGGTCCGATGTGCTGTGAGGCCCTTCCCGCCGGGTGTCATGAGAAACTCCAG 267

Dbb 181 TGCAAGCGGTCCGATGTGCTGTGAGGCCCTTCCCGCCGGGTGTCATGAGAAACTCCAG 240

Qy 268 CTGGGCCCAGAGATCTGCAGCGGGAAAAATCCAAGGCTTATTTATGCCAGGTGAGTGA 327

Dbb 241 CTGGGCCCAGAGATCTGCAGCGGGAAAAATCCAAGGCTTATTTATGCCAGGTGAGTGA 300

Qy 328 TTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 387

Dbb 301 TTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTTTG 360

Qy 388 TCAGGTGTTCTCTCAAAAAATTGGCAGAAGTGGTGAGAAATCCGTATGCCCGCTGAATCTC 447

Dbb 361 TCAGGTGTTCTCTCAAAAAATTGGCAGAAGTGGTGAGAAATCCGTATGCCCGCTGAATCTC 420

Qy 448 CTGGCTGACTTTGCTGGTGGGCCCTTATGTGTGCACTGGGCATTATATGGCTCTTTT 507

Dbb 421 CTGGCTGACTTTGCTGGTGGGCCCTTATGTGTGCACTGGGCATTATATGGCTCTTTT 480

Qy 508 GACCGCACACGCACTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGAACAGCA 567

Dbb 481 GACCGCACACGCACTGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGAACAGCA 540

Qy 568 TATTTAAGTCTTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAGGA 627

Dbb 541 TATTTAAGTCTTTTCTGTGAAAACTCAGAAATCGAGTCTGTGGGAAGCACTCGAGGA 600

Qy 628 CAGAACATGTTGG 640

Dbb 601 CAGAACATGTTGG 613

RESULT 14

BG035606

LOCUS BG035606

DEFINITION 602325670F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413833 5', mRNA sequence.

ACCESSION BG035606

VERSION BG035606.1 GI:12429907

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10140 row: k column: 18
High quality sequence stop: 672.
Location/Qualifiers
1. .812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4413833"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 49.0%; Score 561; DB 4; Length 812;
Best Local Similarity 99.8%; Pred. No. 1.9e-301;
Matches 611; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 TGGAGTGTCCGGCCTGGCCCCCGGCCCGTCTGTGTATGCTCCTGGCTGACTTCGGGG 85
Db 33 TGGAGTGTCCGGCCTGGCCCCCGGCCCGTCTGTGTATGCTCCTGGCTGACTTCGGGG 92
Qy 86 CGCGTGTGTACGCTGGACCGCGCCCGCTCCCGCTACGAGCTGAGCCGCTTGGGCCGGG 145
Db 93 CGCGTGTGTACGCTGGACCGCGCCCGCTCCCGCTACGAGCTGAGCCGCTTGGGCCGGG 152
Qy 146 GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGGCGCTC 205
Db 153 GCAAGCGCTCGCTAGTCTGGACCTGAAGCAGCCCGGGGAGCCCGTGTCTGGCGCTC 212
Qy 206 TGTGCAAGCGGTGGATGTGTCTGGAGCCCTTCCGCCCGGTGTCTATGGAGAACTCC 265
Db 213 TGTGCAAGCGGTGGATGTGTCTGGAGCCCTTCCGCCCGGTGTCTATGGAGAACTCC 272
Qy 266 AGCTGGGCCAGAGATTTCTGACGGGGAATCCAAAGCTTATTTATGCCAGGTGAGTG 325
Db 273 AGCTGGGCCAGAGATTTCTGACGGGGAATCCAAAGCTTATTTATGCCAGGTGAGTG 332
Qy 326 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCAGATATCAACTATTGGCTT 385
Db 333 GATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTGGCCAGATATCAACTATTGGCTT 392
Qy 386 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGATCCGTATGCCCGCTGAATC 445
Db 393 TGTGAGGTGTTCTCTCAAAAATTGGCAGAAAGTGGTGAGATCCGTATGCCCGCTGAATC 452
Qy 446 TCCTGGCTGACTTTGCTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 505
Db 453 TCCTGGCTGACTTTGCTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTT 512
Qy 506 TTGACCGCACACGCACTGGCAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 565
Db 513 TTGACCGCACACGCACTGACAAAGGTCAGGTCAATTGATGCAAAATATGGTGAAGGAACAG 572
Qy 566 CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 625
Db 573 CATATTAAAGTTCTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAG 632
Qy 626 GACAGAACATGT 637
Db 633 GACAGAACATGT 644

RESULT 15

BP318564

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

BP318564 583 bp mRNA linear EST 17-SEP-2004

BP318564 Sugano cDNA library, pericardium Homo sapiens cDNA clone

PCD07986, mRNA sequence.

BP318564

BP318564.1 GI:52247539

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .583

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PCD07986"

/tissue_type="pericardium"

/clone_lib="Sugano cDNA library, pericardium"

Query Match 48.2%; Score 552; DB 5; Length 583;

Best Local Similarity 100.0%; Pred. No. 2e-296;

Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGGCTGGCCCCGGGCGGCTTCTGT 60

Db 32 ATGGCACTGCAGGGCATCTCGGTCTGTGGAGCTGTCGGGCTGGCCCCGGGCGGCTTCTGT 91

Qy 61 GCTATGGTCTGTGCTGCTCGGTCTCGGGCGCGTGTGTACGCTGACCGCCCGGCTCCCGC 120

Db 92 GCTATGGTCTGTGCTGCTCGGTCTCGGGCGCGTGTGTACGCTGACCGCCCGGCTCCCGC 151

Qy 121 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 180

Db 152 TACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGTAGTGTGACCTGAAGCAGCCG 211

Qy 181 CGGGGAGCCCGCTGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 240

Db 212 CGGGGAGCCCGCTGCTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGGAGCCCTTC 271

Qy 241 CGCCCGGCTGTATGGAGAAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAATCCA 300

Db 272 CGCCCGGCTGTATGGAGAAACTCCAGCTGGGCCAGAGATTTCTGACGGGAAATCCA 331

Qy 301 AGGCTTATTTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 360

Db 332 AGGCTTATTTATGCCAGCTGAGTGGATTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCT 391

Qy 361 GGCCACGATATCAACTATTGGCTTTGTGCTGAGTGTCTCTCAAAAATTGGCAGAGTGGT 420

Db 392 GGCCACGATATCAACTATTGGCTTTGTGCTGAGTGTCTCTCAAAAATTGGCAGAGTGGT 451

Qy 421 GAGAAATCCGATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 480

Db 452 GAGAAATCCGATGCCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCTTATGTGT 511

Qy 481 GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGGTCAGGTCATT 540

Db 512 GCACTGGGCATTATAATGGCTCTTTTGTGACCGCACAGCACTGGCAAGGGTCAGGTCATT 571

Qy 541 GATGCAAAATATG 552
| | | | | | | | | |
Db 572 GATGCAAAATATG 583

Search completed: July 27, 2005, 08:08:50
Job time : 4262 secs